

## (12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization  
International Bureau



(43) International Publication Date  
13 November 2003 (13.11.2003)

PCT

(10) International Publication Number  
**WO 03/093464 A1**

(51) International Patent Classification<sup>7</sup>: C12N 9/10, 9/02,  
5/14, 15/82, C07K 14/415, A01H 5/00

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(21) International Application Number: PCT/NZ03/00081

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(22) International Filing Date: 6 May 2003 (06.05.2003)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:  
60/378,930 6 May 2002 (06.05.2002) US  
60/408,782 5 September 2002 (05.09.2002) US

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU,  
AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU,  
CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,  
GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC,  
LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW,  
MX, MZ, NI, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD,  
SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US,  
UZ, VC, VN, YU, ZA, ZM, ZW.

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(84) Designated States (*regional*): ARIPO patent (GH, GM,  
KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW),  
Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM),  
European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE,  
ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO,  
SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM,  
GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

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## Published:

- with international search report
- before the expiration of the time limit for amending the  
claims and to be republished in the event of receipt of  
amendments

*For two-letter codes and other abbreviations, refer to the "Guid-  
ance Notes on Codes and Abbreviations" appearing at the begin-  
ning of each regular issue of the PCT Gazette.*

WO 03/093464 A1

(54) Title: COMPOSITIONS ISOLATED FROM FORAGE GRASSES AND METHODS FOR THEIR USE

(57) Abstract: Isolated polynucleotides encoding polypeptides active in the fructan, cellulose, starch and/or tannin biosynthetic pathways are provided, together with expression vectors and host cells comprising such isolated polynucleotides. Methods for the use of such polynucleotides and polypeptides are also provided.

COMPOSITIONS ISOLATED FROM FORAGE GRASSES  
AND METHODS FOR THEIR USE

5     Technical Field of the Invention

          This invention relates to polynucleotides isolated from forage grass tissues, specifically from *Lolium perenne* (perennial ryegrass) and *Festuca arundinacea* (tall fescue), as well as oligonucleotide probes and primers, genetic constructs comprising the polynucleotides, biological materials (including host cells and plants) incorporating the polynucleotides, polypeptides encoded by the polynucleotides, and methods for using the polynucleotides and polypeptides. More particularly, the invention relates to polypeptides involved in the tannin, cellulose and fructan biosynthetic pathways, and to polynucleotides encoding such polypeptides.

15    Background of the Invention

          Over the past 50 years, there have been substantial improvements in the genetic production potential of ruminant animals (sheep, cattle and deer). Levels of meat, milk or fiber production that equal an animal's genetic potential may be attained within controlled feeding systems, where animals are fully fed with energy dense, conserved forages and grains. However, the majority of temperate farming systems worldwide rely on the *in situ* grazing of pastures. Nutritional constraints associated with temperate pastures can prevent the full expression of an animal's genetic potential. This is illustrated by a comparison between milk production by North American grain-fed dairy cows and New Zealand pasture-fed cattle. North American dairy cattle produce, on average, twice the milk volume of New Zealand cattle, yet the genetic base is similar within both systems (New Zealand Dairy Board and United States Department of Agriculture figures). Significant potential therefore exists to improve the efficiency of conversion of pasture nutrients to animal products through the correction of nutritional constraints associated with pastures.

30    **Carbohydrate metabolism**

          Plant carbohydrates can be divided into two groups depending on their function

within the plant. Structural carbohydrates, such as cellulose and lignin, are usually part of the extracellular matrix. Non-structural, storage carbohydrates act as either long- or short-term carbohydrate stores. Examples of non-structural carbohydrates include starch, sucrose and fructans.

5           Fructans are polymers that are stored in the vacuole and that consist of linear and branched chains of fructose units (for review see Vijn and Smeekens *Plant Physiol.* 120:351-359, 1999). They play an important role in assimilate partitioning and possibly in stress tolerance in many plant families. Grasses use fructans instead of starch as a water-soluble carbohydrate store (Pollock *et al.*, in "Regulation of primary metabolic pathways in plants",  
10 N.J. Kruger *et al.* (eds), Kluwer Academic Publishers, The Netherlands, pp195-226, 1999). Increasing the amount of fructans and sucrose in forage crops leads to an increase in the level of water-soluble carbohydrates and thereby enhances the nutritional value of the plants. In addition, increasing the amount of fructans in forage plants decreases methane production in animals fed the plants, thereby leading to lower greenhouse gas emissions, and decreases  
15 urea production in animals as less protein is degraded in the rumen (Biggs and Hancock *Trends in Plant Sci.*, 6:8-9, 2001). Fructans have also been implicated in protecting plants against water deficits caused by drought or low temperatures. Introduction of enzymes involved in the fructan biosynthetic pathway into plants that do not naturally synthesize fructans may be employed to confer cold tolerance and drought tolerance (Pilon-Smits, *Plant*  
20 *Physiol.* 107:125-130, 1995).

The number of fructose units within a fructan chain is referred to as the degree of polymerization (DP). In grasses, fructans of DP 6-10 are common. Such fructans of low DP are naturally sweet and are therefore of interest for use as sweeteners in foodstuffs. Long fructan chains form emulsions with a fat-like texture and a neutral taste. The human  
25 digestive system is unable to degrade fructans, and fructans of high DP may therefore be used as low-calorie food ingredients. Over-expression of enzymes involved in the fructan biosynthetic pathway may be usefully employed to produce quantities of fructans that can be purified for human consumption.

Five major classes of structurally different fructans have been identified in plants,  
30 with each class showing a different linkage of the fructosyl residues. Fructans found in grasses are of the mixed levan class, consisting of both (2-1)- and (2-6)-linked beta-D-

fructosyl units (Pollock *et al.*, in "Regulation of primary metabolic pathways in plants", N.J. Kruger *et al.* (eds), Kluwer Academic Publishers, The Netherlands, pp195-226, 1999). Fructans are synthesized by the action of fructosyltransferase enzymes on sucrose in the vacuole. These enzymes are closely related to invertases, enzymes that normally hydrolyze sucrose.

Grasses use two fructosyltransferase enzymes to synthesize fructans, namely sucrose:sucrose 1-fructosyltransferase (1-SST) and sucrose:fructan 6-fructosyltransferase (6-SFT) (Pollock *et al.*, in "Regulation of primary metabolic pathways in plants", N.J. Kruger *et al.* (eds), Kluwer Academic Publishers, The Netherlands, pp195-226, 1999). 1-SST is a key enzyme in plant fructan biosynthesis, while 6-SFT catalyzes the formation and extension of beta-2,6-linked fructans that is typically found in grasses. Specifically, 1-SST catalyzes the formation of 1-kestose plus glucose from sucrose, while 6-SFT catalyzes the formation of bifurcose plus glucose from sucrose plus 1-kestose and also the formation of 6-kestose plus glucose from sucrose. Both enzymes can modify 1-kestose, 6-kestose and bifurcose further by adding additional fructose molecules. Over-expression of both 1-SST and 6-SFT in the same plant may be employed to produce fructans for use in human foodstuffs (Sevenier *et al.*, *Nature Biotechnology* 16:843-846; Hellewege *et al.*, *Proc. Nat. Acad. Sci., U.S.A.* 97:8699-8704). For a review of the fructan biosynthetic pathway see Vijn I. and Smeekens S. *Plant Physiol.* 120:351-359, 1999.

The synthesis of sucrose from photosynthetic assimilates in plants, and therefore the availability of sucrose for use in fructan formation, is controlled, in part, by the enzymes sucrose phosphate synthase (SPS) and sucrose phosphate phosphatase (SPP). Sucrose plays an important role in plant growth and development, and is a major end product of photosynthesis. It also functions as a primary transport sugar and in some cases as a direct or indirect regulator of gene expression (for review see Smeekens *Curr. Opin. Plant Biol.* 1:230-234, 1998). SPS regulates the synthesis of sucrose by regulating carbon partitioning in the leaves of plants and therefore plays a major role as a limiting factor in the export of photoassimilates out of the leaf. The activity of SPS is regulated by phosphorylation and moderated by concentration of metabolites and light (Huber *et al.*, *Plant Physiol.* 95:291-297, 1991). Specifically, SPS catalyzes the transfer of glucose from UDP-glucose to fructose-6-phosphate, thereby forming sucrose-6-phosphate (Suc-6-P). Suc-6-P is then



dephosphorylated by SPP to form sucrose (Lunn *et al.*, *Proc. Nat. Acad. Sci., U.S.A.* 97:12914-12919, 2000). The enzymes SPS and SPP exist as a heterotetramer in the cytoplasm of mesophyll cells in leaves, with SPP functioning to regulate SPS activity. SPS is also important in ripening fruits, sprouting tubers and germinating seeds (Laporte *et al.* 5 *Planta* 212:817-822, 2001).

Once in the vacuole, sucrose can be converted into fructan by fructosyltransferases as discussed above, or hydrolyzed into glucose and fructose by the hydrolase enzymes known as invertases (Sturm, *Plant Physiol.* 121:1-7, 1999). There are several different types of invertases, namely extracellular (cell wall), vacuolar (soluble acid) and cytoplasmic, with at 10 least two isoforms of each type of invertase normally being found within a plant species. In addition to having different subcellular locations, the different types of invertases have different biochemical properties. For example, soluble and cell wall invertases operate at acidic pH, whereas cytoplasmic invertases work at a more neutral or alkaline pH. Invertases are believed to regulate the entry of sucrose into different utilization pathways (Grof and 15 Campbell *Aust. J. Plant Physiol.* 28:1-12, 2001). Reduced invertase activity may increase the level of water-soluble carbohydrates in plants. Plants contain several isoforms of cell wall invertases (CWINV), which accumulate as soluble proteins. CWINV plays an important role in phloem unloading and in stress response. *Arabidopsis* contains 9 putative cytoplasmic or neutral invertases that are expressed in all tissues and at all developmental stages implying 20 a more general function than the differentially expressed acid invertases. The neutral invertase cloned from carrot and *Lolium temulentum* show no similarity to acid invertases with the exception of a conserved pentapeptide motif in the grass cDNA (Gallagher *J. Exp. Bot.* 49:789, 1998; Sturm, A. *et al.*, *Physiologia Plantarum*, 107:159-265, 1999).

Another enzyme that acts upon sucrose in plants is soluble sucrose synthase (SUS). 25 Recent results indicate that SUS is localized in the cytosol, associated with the plasma membrane and the actin cytoskeleton. Phosphorylation of SUS is one of the factors controlling localization of the enzyme (Winter and Huber, *Crit. Rev. Biochem. Mol. Biol.* 35:253-89, 2000). It catalyzes the transfer of glucose from sucrose to UDP, yielding UDP-glucose and fructose. Increasing the amount of SUS in a plant increases the amount of 30 cellulose synthesis, whereas decreasing SUS activity should increase fructan levels. Increased SUS concentration may also increase the yield of fruiting bodies. SUS activity is

highest in carbon sink tissues in plants and low in photosynthetic source tissues, and studies have indicated that SUS is the main sucrose-cleaving activity in sink tissues. Grasses have two isoforms of SUS that are encoded by separate genes. These genes are differentially expressed in different tissues.

5           Pyrophosphate-fructose 6-phosphate 1-phosphotransferase (PFP, EC 2.7.1.90) catalyses the reversible conversion of fructose 6-phosphate (Fru-6-P) and pyrophosphate (P<sub>pp</sub>) to fructose 1,6-bisphosphate (Fru-1,6-P) and inorganic phosphate (P<sub>i</sub>). In the plant PFP has important physiological roles in glycosylation, sucrose metabolism, respiratory carbon flow, as well as being a supply of P<sub>pp</sub>. Along with FBPase and PFK, PFP regulates this step  
10 in the pathway of sucrose metabolism. PFP is a cytoplasmic enzyme consisting of a 250kDa tetramer (two alpha and two beta chains) with the two subunits containing all of the regulatory and catalytical functions, respectively. In the plant cell fructose 2-6-bisphosphate is a potent activator of PFP activity. In sugarcane (a C<sub>4</sub> grass), PFP activity is inversely correlated with sucrose content (Whittaker and Botha *Plant Physiol.*, 115, 1651-1659, 1997),  
15 indicating that a reduction of PFP enzyme levels will increase the flux of sucrose synthesis. In forage grasses reducing PFP levels in the leaves will increase water-soluble carbohydrate levels in the leaf tissue. The *Arabidopsis* genome contains four closely related PFP genes thought to encode two isoforms of each subunit, however, only 1 cDNA representing each unit of the purified protein has been isolated from Castor Bean, Potato and Spinach (Todd,  
20 Blakeley and Dennis *Gene*, 152, 181-186, 1995; Carlisle, Blakeley, Hemmingsen, Trevanion, Hiyoshi, Kruger and Dennis *J. Biol. Chem.*, 265, 18366-18371, 1990).

Sucrose Transporters (SUTs) play a major role in the partitioning of disaccharides (sucrose) across membranes (for a review see Williams et al., *Trends Plant Sci.*, 5:283-290, 2000). In particular SUTs are involved in loading and unloading of sucrose into the phloem  
25 and the source-sink relationship within the plant. SUTs are energy dependent and can transport sucrose across large sucrose gradients. In *Arabidopsis* six SUTs have been identified, however in monocots and dicots SUTs form distinct groups. In general, monocots have 2 types of SUTs. For example barley and maize have two SUT proteins, known as SUT1 and SUT2. SUT1 is found in source, not sink, tissues, whereas SUT2 is constitutively  
30 expressed at similar levels in all tissues (Hirose, Imaizumi, Scofield, Furbank and Ohsugi *Plant Cell Physiol.* 38: 1389-1396; 1997; Weschke, et al., *Plant Journal* 21, 455-457, 2000).

Inhibition of SUT1 in potato plants by antisense technology resulted in increased levels of sucrose and starch in the source leaves (Schulz et al. *Planta*, 206, 533-543, 1998). Repressing SUT activity in forage grasses to lower phloem loading in source tissues will increase water soluble carbohydrate content in the leaves.

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### Cellulose synthesis

The major source of dietary fibre for grazing animals comes from plant cell walls. Mammals possess no enzymes capable for breaking down the polysaccharides in plant cell walls. Instead animals such as ruminants depend on microbial breakdown of plant cell walls through fermentation in either the rumen or large intestine.

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Fibre in plants is measured using the Neutral Detergent Fibre (NDF) technique in which plant samples are boiled in a solution containing sodium lauryl sulfate (van Soest *in* "Nutritional Ecology of the Ruminant". Cornell University Press, Ithaca, NY, 1994). This detergent extracts water-soluble components such as sugars, lipids and organic acids. The remaining insoluble residue (fibre) is termed NDF and consists predominantly of plant cell wall components such as cellulose, hemicellulose, and lignin. The amount of cellulose and lignin in cell walls can be determined using the Acid Detergent Fibre (ADF) method where plant samples are boiled in sulfuric acid and sodium lauryl sulfate. The difference between NDF and ADF for a plant sample is normally considered to be the amount of hemicellulose (van Soest *in* "Nutritional Ecology of the Ruminant". Cornell University Press, Ithaca, NY, 1994).

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Stems of most forage species have greater NDF content than leaves. For example, for a temperate C<sub>3</sub> grass in mid-flowering such as tall fescue (*Festuca arundinacea*), NDF content of leaves and stems is 50 and 70%, respectively (Buxton & Redfearn *J. Nutrition* 127:S814-S818, 1997). In contrast, for a C<sub>4</sub> tropical grass such as switchgrass (*Panicum virgatum* L.) the NDF content of leaves and stems is 70 and 85%, respectively. The digestibility of a forage is determined by cell wall content, so that legumes are more digestible than grasses because they contain less NDF. The NDF of a legume, however, is generally less digestible than that of grasses because a higher proportion of the NDF is made up by lignin. The increase of lignin as a component of NDF is also responsible for the decrease in digestibility of grasses at the time of flowering. In fact, ruminants can digest

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only 40-50% of NDF in legumes compared to 60-70% for grass NDF (Buxton & Redfearn *J. Nutrition* 127:S814-S818, 1997). Digestibility of cellulose by ruminants is therefore directly related to the extent of lignification. Generally hemicellulose is more digestible than cellulose.

5 Cellulose is the most abundant carbohydrate in forage making up to 20-40% of dry matter (van Soest *in* "Nutritional Ecology of the Ruminant". Cornell University Press, Ithaca, NY, 1994). The cellulose in forages consists predominantly of  $\beta$ 1-4 glucan (85%) and smaller amounts of pentosans (e.g. xylose and arabinose; 15%). There appear to be two pools of cellulose within the plant cell wall, the difference being one is lignified and the other  
10 is not (van Soest *in* "Nutritional Ecology of the Ruminant". Cornell University Press, Ithaca, NY, 1994). The lignified cellulose is mostly found in the primary cell wall and in the S1 outer layer of the secondary cell wall. Independent of lignification, it appears that cellulose possesses a variability in nutritive quality (van Soest *in* "Nutritional Ecology of the Ruminant". Cornell University Press, Ithaca, NY, 1994). This indicates that it is possible to  
15 alter the rate of cellulose digestibility by modifying the chemical composition of cellulose. This could be achieved through manipulating the actions of the cellulose synthesis and cellulose synthesis-like enzymes found in plant cells. One method to increase digestibility in this way is to increase the activity of the cellulose synthesis and cellulose synthesis-like enzymes responsible for synthesizing hemicellulose or to down regulate the cellulose  
20 synthesis and cellulose synthesis-like enzymes making cellulose. Hemicellulose is much more digestible than cellulose and is less likely to become lignified. Another way of manipulating cell wall composition is through modifying the rate and supply of primary components required for cellulose synthesis, i.e. of  $\beta$ 1-4 glucan and pentosans such as xylose and arabinose. One way to achieve this is to modify the actions of soluble sucrose synthase  
25 and UDP glucose pyrophosphorylase (UDP-GP) enzymes that produce the UDP-glucose required for cellulose synthesis. This may be further modified by manipulating the actions of the large and small subunits of ADP-glucose pyrophosphorylase (ADP-GP), the two enzymes that are rate-limiting steps in starch synthesis (Smith, Denyer and Martin *Ann. Rev. Plant Phys. Plant Mol. Biol.* 48:67-87, 1997).

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Manipulating expression of the UDPGP and ADP-GP genes would alter the chemical composition of plant cell walls in forage plants. Altering cell wall biosynthesis therefore provides an opportunity to increase digestibility of the plant dry matter. This may be achieved by increasing the amount of carbon in the plant allocated to cellulose biosynthesis at the expense of lignin biosynthesis. Alternatively, decreasing the amount of cellulose biosynthesis and increasing the amount of water-soluble carbohydrates would have a similar effect. Furthermore, specifically increasing hemicellulose levels in the plant cell walls at expense of cellulose would also increase forage digestibility. By utilizing specific promoters in combination with the UDPGP and ADP-GP genes it is possible to increase or decrease the starch, cellulose and/or hemicellulose levels in the leaf or stem.

### **Tannin Biosynthetic Pathway**

Condensed tannins are polymerized flavonoids. More specifically, tannins are composed of catechin 4-ol and catechin monomer units, and are stored in the vacuole. In many temperate forage crops, such as ryegrass and fescue, foliar tissues are tannin-negative. This leads to a high initial rate of fermentation when these crops are consumed by ruminant livestock resulting in both protein degradation and production of ammonia by the livestock. These effects can be reduced by the presence of low to moderate levels of tannin. In certain other plant species, the presence of high levels of tannins reduces palatability and nutritive value. Introduction of genes encoding enzymes involved in the biosynthesis of condensed tannins into a plant may be employed to synthesize flavonoid compounds that are not normally made in the plant. These compounds may then be isolated and used for treating human or animal disorders or as food additives.

Much of the biosynthetic pathway for condensed tannins is shared with that for anthocyanins, which are pigments responsible for flower color. Therefore, modulation of the levels of enzymes involved in the tannin biosynthetic pathway may be employed to alter the color of foliage and the pigments produced in flowers.

Most tannins described to date contain pro-cyanidin units derived from dihydroquercetin and pro-delphinidin units derived from dihydromyricetin. However, some tannins contain pro-pelargonidin units derived from dihydrokaempferol. The initial step in the tannin biosynthetic pathway is the condensation of coumaryl CoA with malonyl CoA to

give naringenin-chalcone, which is catalyzed by the enzyme chalcone synthase (CHS). The enzyme chalcone isomerase (CHI) catalyzes the isomerization of naringenin chalcone to naringenin (also known as flavanone), which is then hydroxylated by the action of the enzyme flavonone 3- beta-hydroxylase (F3 $\beta$ H) to give dihydrokaempferol. The enzyme  
5 flavonoid 3'-hydroxylase (F3'OH) catalyzes the conversion of dihydrokaempferol to dihydroquercetin, which in turn can be converted into dihydromyricetin by the action of flavonoid 3'5'-hydroxylase (F3'5'OH). F3'OH is a P450 enzyme responsible for the brick red to orange pelargonidin-based pigments, whereas F3'5'OH is responsible for the purple and blue delphinidin-based pigments. The enzyme dihydroflavonol-4-reductase (DFR)  
10 catalyzes the last step before dihydrokaempferol, dihydroquercetin and dihydromyricetin are committed for either anthocyanin (flower pigment) or proanthocyanidin (condensed tannin) formation. DFR also converts dihydrokaempferol to afzelchin-4-ol, dihydroquercetin to catechin-4-ol, and dihydromyricetin to gallocatechin-4-ol, probably by the action of more than one isoform. For a review of the tannin biosynthetic pathway, see, Robbins M.P. and  
15 Morris P. in *Metabolic Engineering of Plant Secondary Metabolism*, Verpoorte and Alfermann (eds), Kluwer Academic Publishers, the Netherlands, 2000. The leucoanthocyanidin dioxygenase (LDOX) enzyme belongs to the iron/ascorbate-dependent family of oxidoreductases. In maize the LDOX gene A2 is required for the oxidation of leucoanthocyanidins into anthocyanidins (Menssen, Hoehmann, Martin, Schnable, Peterson,  
20 Saedler and Gierl *EMBO J.* 9:3051-3057, 1990).

While polynucleotides encoding some of the enzymes involved in the fructan, cellulose and tannin biosynthetic pathways have been isolated for certain species of plants, genes encoding many of the enzymes in a wide range of plant species have not yet been  
25 identified. Thus there remains a need in the art for materials useful in the modification of fructan and tannin content and composition in plants, and for methods for their use.

#### Summary of the Invention

The present invention provides enzymes involved in the fructan, cellulose, starch  
30 and/or tannin biosynthetic pathways that are encoded by polynucleotides isolated from forage grass tissues. The polynucleotides were isolated from *Lolium perenne* (perennial ryegrass)

and *Festuca arundinacea* (tall fescue) tissues taken at different times of the year, specifically in winter and spring, and from different parts of the plants, including: leaf blades, leaf base, pseudostems, roots and stems. Genetic constructs, expression vectors and host cells comprising the inventive polynucleotides are also provided, together with methods for using  
5 the inventive polynucleotides and genetic constructs to modulate the biosynthesis of fructans and tannins.

In specific embodiments, the isolated polynucleotides of the present invention comprise a sequence selected from the group consisting of: (a) SEQ ID NO: 1-44; (b) complements of SEQ ID NO: 1-44; (c) reverse complements of SEQ ID NO: 1-44; (d)  
10 reverse sequences of SEQ ID NO: 1-44; (e) sequences having a 99% probability of being functionally or evolutionarily related to a sequence of (a)-(d), determined as described below; and (f) sequences having at least 75%, 80%, 90%, 95% or 98% identity to a sequence of (a)-(d), the percentage identity being determined as described below. Polynucleotides comprising at least a specified number of contiguous residues ("x-mers") of any of SEQ ID  
15 NO: 1-44, and oligonucleotide probes and primers corresponding to SEQ ID NO: 1-44 are also provided. All of the above polynucleotides are referred to herein as "polynucleotides of the present invention."

In further aspects, the present invention provides isolated polypeptides encoded by the inventive polynucleotides. In specific embodiments, such polypeptides comprise an  
20 amino acid sequence of SEQ ID NO: 45-88. The present invention also provides polypeptides comprising a sequence having at least 75%, 80%, 90%, 95% or 98% identity to a sequence of SEQ ID NO: 45-88, wherein the polypeptide possesses the same functional activity as the polypeptide comprising a sequence of SEQ ID NO: 45-88. The present invention also contemplates isolated polypeptides comprising at least a functional portion of  
25 an amino acid sequence selected from the group consisting of: (a) SEQ ID NO: 45-88; and (b) sequences having at least 75%, 80%, 90%, 95% or 98% identity to a sequence of SEQ ID NO: 45-88.

In another aspect, the present invention provides genetic constructs, or expression vectors, comprising a polynucleotide of the present invention, either alone, in combination  
30 with one or more of the inventive sequences, or in combination with one or more known polynucleotides.

In certain embodiments, the present invention provides genetic constructs comprising, in the 5'-3' direction: a gene promoter sequence; an open reading frame coding for at least a functional portion of a polypeptide of the present invention; and a gene termination sequence. An open reading frame may be orientated in either a sense or anti-sense direction. Genetic constructs comprising a non-coding region of a polynucleotide of the present invention or a polynucleotide complementary to a non-coding region, together with a gene promoter sequence and a gene termination sequence, are also provided. Preferably, the gene promoter and termination sequences are functional in a host cell, such as a plant cell. Most preferably, the gene promoter and termination sequences are those of the original enzyme genes but others generally used in the art, such as the Cauliflower Mosaic Virus (CMV) promoter, with or without enhancers, such as the Kozak sequence or Omega enhancer, and the *Agrobacterium tumefaciens* nopal synthase terminator may be usefully employed in the present invention. Tissue-specific promoters may be employed in order to target expression to one or more desired tissues. The construct may further include a marker for the identification of transformed cells.

In a further aspect, transgenic cells, such as transgenic plant cells, comprising the genetic constructs of the present invention are provided, together with tissues and plants comprising such transgenic cells, and fruits, seeds and other products, derivatives, or progeny of such plants.

In yet another aspect, the present invention provides methods for modulating the fructan, cellulose, starch and/or tannin content and composition of a target organism, such as a plant, by modulating the amount and/or activity of an inventive polynucleotide or polypeptide in the organism. In certain embodiments, such methods include stably incorporating into the genome of the target plant a genetic construct of the present invention. In a preferred embodiment, the target plant is a forage grass, preferably selected from the group consisting of *Lolium* and *Festuca* species, and most preferably from the group consisting of *Lolium perenne* and *Festuca arundinacea*.

In a related aspect, methods for producing a plant having altered fructan or tannin composition is provided. Such methods comprise modulating the amount and/or activity of an inventive polynucleotide or polypeptide in a plant cell by, for example, transforming a plant cell with a genetic construct of the present invention to provide a transgenic cell, and



cultivating the transgenic cell under conditions conducive to regeneration and mature plant growth.

In yet a further aspect, the present invention provides methods for modifying the activity of an enzyme in a target organism, such as a plant, comprising modulating the amount and/or activity of an inventive polynucleotide or polypeptide in the target organism by, for example stably incorporating into the genome of the target organism a genetic construct of the present invention. In a preferred embodiment, the target plant is a forage grass, preferably selected from the group consisting of *Lolium* and *Festuca* species, and most preferably from the group consisting of *Lolium perenne* and *Festuca arundinacea*.

#### Brief Description of the Figures

Fig. 1 shows the neutral invertase activity of the recombinant grass alkaline/neutral invertase protein AN\_INV8 from *L. perenne* (amino acid sequence provided in SEQ ID NO: 56; cDNA sequence provided in SEQ ID NO: 12). Activity was measured as the  $\mu\text{g}$  of glucose release from cleavage of sucrose per hour at pH 7. Also shown is an empty vector negative control (pET41a).

Fig. 2 shows the PFP activity of *L. perenne* and *F. arundinacea* PFPA and PFPB subunits in coupled reactions. Amino acid sequences for *L. perenne* PFPA and PFPB are given in SEQ ID NO: 59 and 62, respectively (corresponding cDNA sequences are SEQ ID NO: 15 and 18), and amino acid sequences for *F. arundinacea* PFPA and PFPB are given in SEQ ID NO: 60 and 63, respectively (corresponding cDNA sequences are SEQ ID NO: 16 and 19). Oxidation of NADH was measured as nmoles PPi converted.

Fig. 3 shows the amino acid sequence of SEQ ID NO: 45. The conserved UTP-glucose-1-phosphate uridylyltransferase domain is underlined.

Fig. 4 shows the amino acid sequence of SEQ ID NO: 46. The conserved UTP-glucose-1-phosphate uridylyltransferase domain is underlined.

Fig. 5 shows the amino acid sequence of SEQ ID NO: 47. The conserved glycoside hydrolase, family 32 domain is underlined.

Fig. 6 shows the amino acid sequence of SEQ ID NO: 48. A transmembrane domain is underlined.

Fig. 7 shows the amino acid sequence of SEQ ID NO: 53. The signal peptide is in bold/italics.

Fig. 8 shows the amino acid sequence of SEQ ID NO: 54. The signal peptide is in bold/italics and two conserved Antifreeze protein, type I domains are underlined.

5 Fig. 9 shows the amino acid sequence of SEQ ID NO: 55. The signal peptide is in bold/italics.

Fig. 10 shows the amino acid sequence of SEQ ID NO: 56. Two transmembrane domains are double underlined.

10 Fig. 11 shows the amino acid sequence of SEQ ID NO: 57. Two transmembrane domains are double underlined.

Fig. 12 shows the amino acid sequence of SEQ ID NO: 58. Two transmembrane domains are double underlined.

15 Fig. 13 shows the amino acid sequence of SEQ ID NO: 59. The conserved phosphofructokinase domain is underlined and a transmembrane domain is double underlined.

Fig. 14 shows the amino acid sequence of SEQ ID NO: 60. The conserved phosphofructokinase domain is underlined and a transmembrane domain is double underlined.

20 Fig. 15 shows the amino acid sequence of SEQ ID NO: 61. The conserved phosphofructokinase is underlined.

Fig. 16 shows the amino acid sequence of SEQ ID NO: 62. The conserved phosphofructokinase domain is underlined.

Fig. 17 shows the amino acid sequence of SEQ ID NO: 63. The conserved phosphofructokinase domain is underlined.

25 Fig. 18 shows the amino acid sequence of SEQ ID NO: 64. The conserved glycosyl transferase, group 1 domain is underlined and two transmembrane domains are double underlined.

30 Fig. 19 shows the amino acid sequence of SEQ ID NO: 65. The conserved glycosyl transferase, group 1 domain is underlined and two transmembrane domains are double underlined.

Fig. 20 shows the amino acid sequence of SEQ ID NO: 66. The conserved substrate transporter domain is in bold and eleven transmembrane domains are double underlined.

Fig. 21 shows the amino acid sequence of SEQ ID NO: 67. Nine transmembrane domains are double underlined.

5 Fig. 22 shows the amino acid sequence of SEQ ID NO: 68. The conserved substrate transporter domain is in bold and eleven transmembrane domains are double underlined.

Fig. 23 shows the amino acid sequence of SEQ ID NO: 69. The conserved substrate transporter domain is in bold and eleven transmembrane domains are double underlined.

10 Fig. 24 shows the amino acid sequence of SEQ ID NO: 70. The conserved substrate transporter domain is in bold and eleven transmembrane domains are double underlined.

Fig. 25 shows the amino acid sequence of SEQ ID NO: 72. The conserved nucleotidyl transferase domain is in bold and three ADP-glucose pyrophosphorylase are boxed. Nine transmembrane domains are double underlined.

15 Fig. 26 shows the amino acid sequence of SEQ ID NO: 73. The conserved nucleotidyl transferase domain is in bold and three ADP-glucose pyrophosphorylase domains are boxed. A transmembrane domain is double underlined.

Fig. 27 shows the amino acid sequence of SEQ ID NO: 74. The conserved nucleotidyl transferase domain is in bold and three ADP-glucose pyrophosphorylase domains are boxed. A transmembrane domain is double underlined.

20 Fig. 28 shows the amino acid sequence of SEQ ID NO: 75. The conserved nucleotidyl transferase domain is in bold and three ADP-glucose pyrophosphorylase domains are boxed. The signal peptide is in bold/italics and a transmembrane domain is double underlined.

25 Fig. 29 shows the amino acid sequence of SEQ ID NO: 76. The conserved naringenin-chalcone synthase domain is underlined. The signal peptide is in bold/italics and a transmembrane domain is double underlined.

Fig. 30 shows the amino acid sequence of SEQ ID NO: 77. The conserved naringenin-chalcone synthase domain is underlined and two transmembrane domains are double underlined.

Fig. 31 shows the amino acid sequence of SEQ ID NO: 78. The conserved naringenin-chalcone synthase domain is underlined and two transmembrane domains are double underlined.

5 Fig. 32 shows the amino acid sequence of SEQ ID NO: 79. A transmembrane domain is double underlined.

Fig. 33 shows the amino acid sequence of SEQ ID NO: 80. A transmembrane domain is double underlined.

Fig. 34 shows the amino acid sequence of SEQ ID NO: 81. A transmembrane domain is double underlined.

10 Fig. 35 shows the amino acid sequence of SEQ ID NO: 82. The conserved Cytochrome P450 domain is underlined and three transmembrane domains are double underlined.

Fig. 36 shows the amino acid sequence of SEQ ID NO: 83. The conserved Cytochrome P450 domain is boxed, the signal peptide is in bold and a transmembrane domain is double underlined.

Fig. 37 shows the amino acid sequence of SEQ ID NO: 84. The conserved Cytochrome P450 domain is boxed and three transmembrane domains are double underlined.

Fig. 38 shows the amino acid sequence of SEQ ID NO: 85. The conserved Cytochrome P450 domain is boxed, the signal peptide is in bold/italics and three transmembrane domains are double underlined.

Fig. 39 shows the amino acid sequence of SEQ ID NO: 86. The conserved Cytochrome P450 domain is boxed and three transmembrane domains are double underlined.

Fig. 40 shows the amino acid sequence of SEQ ID NO: 87. The conserved Cytochrome P450 domain is boxed, the signal peptide is in bold/italics and three transmembrane domains are double underlined.

Fig. 41 shows the amino acid sequence of SEQ ID NO: 88. The conserved 2OG-Fe(II) oxygenase superfamily domain is underlined.

#### Detailed Description of the Invention

30 The polypeptides of the present invention, and the polynucleotides encoding such polypeptides, have activity in fructan, cellulose, starch and/or tannin biosynthetic pathways

in plants. Using the methods and materials of the present invention, the fructan, cellulose, starch and/or tannin content of a plant may be modulated by modulating expression of polynucleotides of the present invention, or by modifying the activity of the polynucleotides or polypeptides encoded by the polynucleotides. The isolated polynucleotides and polypeptides of the present invention may thus be usefully employed in the correction of nutritional imbalances associated with temperate pastures and to increase the yield of animal products from pastures.

The fructan, cellulose, starch and/or tannin content of a target organism, such as a plant, may be modified, for example, by incorporating additional copies of genes encoding enzymes involved in the fructan, cellulose, starch and/or tannin biosynthetic pathways into the genome of the target plant. Similarly, a modified fructan, cellulose, starch and/or tannin content can be obtained by transforming the target plant with anti-sense copies of such genes. In addition, the number of copies of genes encoding for different enzymes in the fructan, cellulose, starch and tannin biosynthetic pathways can be manipulated to modify the relative amount of each monomer unit synthesized, thereby leading to the formation of fructans, cellulose, starch or tannins having altered composition.

The present invention thus provides methods for modulating the polynucleotide and/or polypeptide content and composition of an organism. In certain embodiments, such methods involve stably incorporating into the genome of the organism a genetic construct comprising one or more polynucleotides of the present invention. In one embodiment, the target organism is a plant species, preferably a forage plant, more preferably a grass of the *Lolium* or *Festuca* species, and most preferably *Lolium perenne* or *Festuca arundinacea*. In related aspects, methods for producing a plant having an altered genotype or phenotype is provided, such methods comprising transforming a plant cell with a genetic construct of the present invention to provide a transgenic cell, and cultivating the transgenic cell under conditions conducive to regeneration and mature plant growth. Plants having an altered genotype or phenotype as a consequence of modulation of the level or content of a polynucleotide or polypeptide of the present invention compared to a wild-type organism, as well as components (seeds, etc.) of such plants, and the progeny of such plants, are contemplated by and encompassed within the present invention.

The isolated polynucleotides of the present invention additionally have utility in genome mapping, in physical mapping, and in positional cloning of genes. The polynucleotide sequences identified as SEQ ID NOS: 1-44 and their variants, may also be used to design oligonucleotide probes and primers. Oligonucleotide probes and primers have sequences that are substantially complementary to the polynucleotide of interest over a certain portion of the polynucleotide, preferably over substantially the entire length of the polynucleotides. Oligonucleotide probes designed using the inventive polynucleotides may be employed to detect the presence and examine the expression patterns of genes in any organism having sufficiently similar DNA and RNA sequences in their cells using techniques that are well known in the art, such as slot blot DNA hybridization techniques. Oligonucleotide primers designed using the polynucleotides of the present invention may be used for PCR amplifications. Oligonucleotide probes and primers designed using the inventive polynucleotides may also be used in connection with various microarray technologies, including the microarray technology of Affymetrix (Santa Clara, CA).

In a first aspect, the present invention provides isolated polynucleotide sequences identified in the attached Sequence Listing as SEQ ID NOS: 1-44, and polypeptide sequences identified in the attached Sequence Listing as SEQ ID NO: 45-88. The polynucleotides and polypeptides of the present invention have demonstrated similarity to the following polypeptides that are known to be involved in fructan, cellulose, starch and/or tannin biosynthetic processes:

TABLE 1

SEQ ID NO: DNA	SEQ ID NO: polypeptide	Category	Description
1, 2	45, 46	Carbohydrate metabolism	Homolog of UDP-glucose pyrophosphorylase (EC 2.7.7.9) (UDPGP or UGPASE) which is one of the key enzymes of the carbohydrate metabolic pathway. It plays a central role as glucosyl donor in cellular metabolic pathways. UDP-glucose pyrophosphorylase catalyzes the reversible uridylyl transfer from UDP-glucose to MgPPi, forming glucose 1-phosphate and MgUTP.
3, 4	47, 48	Fructan	Homolog of Sucrose (Suc):Suc 1-fructosyl-

SEQ ID NO: DNA	SEQ ID NO: polypeptide	Category	Description
		metabolism	transferase (1-SST) isolated from <i>L. perenne</i> . 1-SST is the key enzyme in plant fructan biosynthesis and catalyzes the <i>de novo</i> fructan synthesis from sucrose. Fructans play an important role in assimilation partitioning and in stress tolerance in many plants. It contains a typical signature of the glycosyl hydrolases family 32. The glycosyl hydrolases family 32 domain signature has a consensus of HYQPxxH/NxxNDPNG, where D is the active site residue (Henrissat, <i>Biochem. J.</i> 280:309-316, 1991).
5-14	49-58	Fructan metabolism	Homolog of alkaline/neutral invertase (AN-INV) that is involved in catalyzing sucrose into hexoses for utilization as a source of carbon and energy. AN-INV belongs to the family 32 of glycosyl hydrolases. Neutral invertase is an octamer of 456 kDa with subunits of 57 kDa, whereas alkaline invertase is a 504 kDa tetramer with subunits of 126 kDa. Neutral invertase also hydrolyzes raffinose and stachyose and, therefore, is a beta-fructo-furanosidase. In contrast, alkaline invertase is highly specific for sucrose (Lee and Sturm, <i>Plant Physiol.</i> 112:1513-1522, 1996).
15, 16	59, 60	Fructan metabolism	Homologue of the alpha subunit of Pyrophosphate-dependent 6-phosphofructo-1-phosphotransferase (PFPA) that plays a role in carbohydrate metabolism. PFP is involved in the first step of glycolysis in the phosphorylation of fructose 6-phosphate (Fru 6-P). PFPA acts as a regulatory protein in regulating both the catalytic activity and the Fru-2,6-P <sub>2</sub> -binding affinity of the beta subunit (Siebers <i>et al.</i> , <i>J. Bacteriol.</i> 180:2137-2143, 1998).
17-19	61-63	Fructan metabolism	Homolog of the beta subunit of Pyrophosphate-dependent 6-phosphofructo-1-phosphotransferase (PFPB) which plays a role in carbohydrate metabolism. PFP is involved in the first step of glycolysis in the phosphorylation of fructose 6-phosphate (Fru-6-P). The catalytic activity of the PFP enzyme is associated with the beta subunit PFPB while

SEQ ID NO: DNA	SEQ ID NO: polypeptide	Category	Description
			PFPA acts as a regulatory protein in regulating both the catalytic activity and the Fru-2,6-P <sub>2</sub> -binding affinity of the beta subunit (Carlisle <i>et al.</i> , <i>J. Biol. Chem.</i> 265:18366-18371, 1990; Siebers <i>et al.</i> , <i>J. Bacteriol.</i> 180:2137-2143, 1998).
20, 21	64, 65	Fructan metabolism	Homologue of sucrose phosphate synthase which is involved in the sucrose synthesis pathway. Sucrose plays an important role in plant growth and development and is a major end product of photosynthesis. It also functions as a primary transport sugar and in some cases as a direct or indirect regulator of gene expression. SPS-1 regulates the synthesis of sucrose by regulating carbon partitioning in the leaves of plants and therefore plays a major role as a limiting factor in the export of photoassimilates out of the leaf. The activity of SPS is regulated by phosphorylation and moderated by concentration of metabolites and light.
22-24	66-68	Fructan metabolism	Homologue of the sugar transporter SUT1, a member of the SUT family of low- and high-affinity sucrose transporters that is involved in transport of sucrose from mature leaves via the phloem. Expression of SUT1 has also been observed in other tissues (stems and parts of flower) suggesting that SUT1 may also have other functions, such as sucrose retrieval and phloem unloading (Burkle <i>et al.</i> , <i>Plant Physiol.</i> 118:59-68, 1998).
25, 26	69, 70	Fructan metabolism	Homologue of sugar transporter SUT2, a member of the SUT family of low- and high-affinity sucrose transporters. SUT2 is more highly expressed in sink than in source leaves, is inducible by sucrose and regulates the relative activity of low- and high-affinity sucrose transport into sieve elements (Barker <i>et al.</i> , <i>Plant Cell</i> 12:1153-1164, 2000).
27	71	Fructan metabolism	Homologue of a sugar transporter, a member of the SUT family of low- and high-affinity sucrose transporters that is involved in transport of sucrose from mature leaves via the phloem.
28, 29	72, 73	Fructan	Homolog of the large subunit (LSU) of ADP-



SEQ ID NO: DNA	SEQ ID NO: polypeptide	Category	Description
		metabolism	glucose pyrophosphorylase (AGPase), which plays a role in starch biosynthesis. It catalyzes the synthesis of the activated glycosyl donor, ADP-glucose from glucose-1-phosphate and ATP. The enzyme is found in chloroplasts of leaves and amyloplasts of developing endosperm. AGPase belongs to the glucose-1-phosphate adenylyltransferase family.
30, 31	74, 75	Carbohydrate metabolism	Homolog of the small subunit (SSU) of ADP-glucose pyrophosphorylase (AGPase), which plays a role in starch biosynthesis. It catalyzes the synthesis of the activated glycosyl donor, ADP-glucose from glucose-1-phosphate and ATP. The enzyme is found in chloroplasts of leaves and amyloplasts of developing endosperm. AGPase belongs to the glucose-1-phosphate adenylyltransferase family.
32, 33	76, 77	Tannin biosynthesis	Homolog of Chalcone Synthase (CHS) which is an important enzyme in flavonoid synthesis.
34-37	78-81	Tannin metabolism	Homologue of dihydroflavonol-4-reductase (DFR) that belongs to the dihydroflavonol-4-reductases family and is involved in the flavonoid synthesis and anthocyanidins biosynthesis. Flavonoids are secondary metabolites derived from phenylalanine and acetate metabolism that perform a variety of essential functions in higher plants.
38-43	82-87	Tannin metabolism	Homologue of flavonoid 3'-hydroxylase (F3'H) which is a key enzyme in the flavonoid pathway leading to the production of the colored anthocyanins where it is involved in determination of flower coloring. Anthocyanins synthesized in plants are controlled by flavonoid 3'-hydroxylase and flavonoid 3',5'-hydroxylase which are members of the cytochrome P450 family, a large group of membrane-bound heme-containing enzymes that are involved in a range of NADPH- and O <sub>2</sub> -dependent hydroxylation reactions. Plants have evolved a large number of different P450 enzymes for the synthesis of secondary metabolites. The F3 'H transcript is most abundant in petals from flowers at an early stage of development and levels decline as the

SEQ ID NO: DNA	SEQ ID NO: polypeptide	Category	Description
			flower matures. Transcripts are also detected in the ovaries, sepals, peduncles, stems and anthers of the petunia plant (Brugliera <i>et al.</i> , <i>Plant J.</i> 19:441-451, 1999
44	88	Tannin biosynthesis	Homologue of leucoanthocyanidin dioxygenase (LDOX) which is an enzyme in the flavonoid biosynthesis pathway. LDOX is expressed as a late gene in the flavonoid biosynthesis pathway.

All the polynucleotides and polypeptides provided by the present invention are isolated and purified, as those terms are commonly used in the art. Preferably, the polypeptides and polynucleotides are at least about 80% pure, more preferably at least about 90% pure, and most preferably at least about 99% pure.

The word "polynucleotide(s)," as used herein, means a polymeric collection of nucleotides, and includes DNA and corresponding RNA molecules and both single and double stranded molecules, including HnRNA and mRNA molecules, sense and anti-sense strands of DNA and RNA molecules, and comprehends cDNA, genomic DNA, and wholly or partially synthesized polynucleotides. A polynucleotide of the present invention may be an entire gene, or any portion thereof. As used herein, a "gene" is a DNA sequence which codes for a functional protein or RNA molecule. Operable anti-sense polynucleotides may comprise a fragment of the corresponding polynucleotide, and the definition of "polynucleotide" therefore includes all operable anti-sense fragments. Anti-sense polynucleotides and techniques involving anti-sense polynucleotides are well known in the art and are described, for example, in Robinson-Benion *et al.*, *Methods in Enzymol.* 254(23): 363-375, 1995 and Kawasaki *et al.*, *Artific. Organs* 20(8): 836-848, 1996.

In specific embodiments, the present invention provides isolated polynucleotides comprising a sequence of SEQ ID NO: 1-44; polynucleotides comprising variants of SEQ ID NO: 1-44; polynucleotides comprising extended sequences of SEQ ID NO: 1-44 and their variants, oligonucleotide primers and probes corresponding to the sequences set out in SEQ ID NO: 1-44 and their variants, polynucleotides comprising at least a specified number of contiguous residues of any of SEQ ID NO: 1-44 (*x*-mers), and polynucleotides comprising extended sequences which include portions of the sequences set out in SEQ ID NO: 1-44, all

of which are referred to herein, collectively, as “polynucleotides of the present invention.” Polynucleotides that comprise complements of such polynucleotide sequences, reverse complements of such polynucleotide sequences, or reverse sequences of such polynucleotide sequences, together with variants of such sequences, are also provided.

5 The definition of the terms “complement(s),” “reverse complement(s),” and “reverse sequence(s),” as used herein, is best illustrated by the following example. For the sequence 5’ AGGACC 3’, the complement, reverse complement, and reverse sequence are as follows:

complement	3’ TCCTGG 5’
reverse complement	3’ GGTCCT 5’
10 reverse sequence	5’ CCAGGA 3’.

Preferably, sequences that are complements of a specifically recited polynucleotide sequence are complementary over the entire length of the specific polynucleotide sequence.

As used herein, the term “x-mer,” with reference to a specific value of “x,” refers to a polynucleotide comprising at least a specified number (“x”) of contiguous residues of: any of  
15 the polynucleotides provided in SEQ ID NO: 1-44. The value of x may be from about 20 to about 600, depending upon the specific sequence.

Polynucleotides of the present invention comprehend polynucleotides comprising at least a specified number of contiguous residues (x-mers) of any of the polynucleotides identified as SEQ ID NO: 1-44, or their variants. Similarly, polypeptides of the present  
20 invention comprehend polypeptides comprising at least a specified number of contiguous residues (x-mers) of any of the polypeptides identified as SEQ ID NO: 45-88. According to preferred embodiments, the value of x is at least 20, more preferably at least 40, more preferably yet at least 60, and most preferably at least 80. Thus, polynucleotides of the present invention include polynucleotides comprising a 20-mer, a 40-mer, a 60-mer, an 80-  
25 mer, a 100-mer, a 120-mer, a 150-mer, a 180-mer, a 220-mer, a 250-mer; or a 300-mer, 400-mer, 500-mer or 600-mer of a polynucleotide provided in SEQ ID NO: 1-44, or a variant of one of the polynucleotides corresponding to the polynucleotides provided in SEQ ID NO: 1-44. Polypeptides of the present invention include polypeptides comprising a 20-mer, a 40-mer, a 60-mer, an 80-mer, a 100-mer, a 120-mer, a 150-mer, a 180-mer, a 220-mer, a 250-  
30 mer; or a 300-mer, 400-mer, 500-mer or 600-mer of a polypeptide provided in SEQ ID NO: 45-88, or a variant thereof.

The polynucleotides of the present invention were isolated by high throughput sequencing of cDNA libraries prepared from forage grass tissue collected from *Lolium perenne* and *Festuca arundinacea*. Some of the polynucleotides of the present invention may be "partial" sequences, in that they do not represent a full-length gene encoding a full-length polypeptide. Such partial sequences may be extended by analyzing and sequencing various DNA libraries using primers and/or probes and well known hybridization and/or PCR techniques. Partial sequences may be extended until an open reading frame encoding a polypeptide, a full-length polynucleotide and/or gene capable of expressing a polypeptide, or another useful portion of the genome is identified. Such extended sequences, including full-length polynucleotides and genes, are described as "corresponding to" a sequence identified as one of the sequences of SEQ ID NO: 1-44 or a variant thereof, or a portion of one of the sequences of SEQ ID NO: 1-44 or a variant thereof, when the extended polynucleotide comprises an identified sequence or its variant, or an identified contiguous portion (x-mer) of one of the sequences of SEQ ID NO: 1-44 or a variant thereof. Similarly, RNA sequences, reverse sequences, complementary sequences, anti-sense sequences and the like, corresponding to the polynucleotides of the present invention, may be routinely ascertained and obtained using the cDNA sequences identified as SEQ ID NO: 1-44.

The polynucleotides identified as SEQ ID NOS: 1-44 contain open reading frames ("ORFs") encoding polypeptides and functional portions of polypeptides. Open reading frames may be identified using techniques that are well known in the art. These techniques include, for example, analysis for the location of known start and stop codons, most likely reading frame identification based on codon frequencies, etc. Suitable tools and software for ORF analysis are well known in the art and include, for example, GeneWise, available from The Sanger Center, Wellcome Trust Genome Campus, Hinxton, Cambridge, CB10 1SA, United Kingdom; Diogenes, available from Computational Biology Centers, University of Minnesota, Academic Health Center, UMHG Box 43 Minneapolis MN 55455; and GRAIL, available from the Informatics Group, Oak Ridge National Laboratories, Oak Ridge, Tennessee TN. Once a partial open reading frame is identified, the polynucleotide may be extended in the area of the partial open reading frame using techniques that are well known in the art until the polynucleotide for the full open reading frame is identified.

The location of ORFs (by nucleotide position) contained within SEQ ID NO: 1-44, and the corresponding amino acid sequences are provided in Table 2 below.

TABLE 2

5

SEQ ID NO: Polynucleotide	ORF	SEQ ID NO: Polypeptide
1	72-1493	45
2	66-1481	46
3	0-1607	47
4	1-1914	48
5	123-1934	49
6	0-1671	50
7	114-1979	51
8	0-737	52
9	47-1783	53
10	170-2029	54
11	113-1849	55
12	154-1818	56
13	211-1866	57
14	79-1767	58
15	76-1926	59
16	80-1930	60
17	91-1782	61
18	91-1782	62
19	84-1775	63
20	97-2994	64
21	112-3065	65
22	226-1794	66
23	0-1226	67
24	243-1811	68
25	207-1727	69
26	101-1615	70
27	108-1634	71
28	150-1718	72
29	169-1737	73
30	12-1589	74
31	5-1579	75
32	136-1332	76
33	136-1332	77
34	95-836	78
35	95-1123	79

SEQ ID NO: Polynucleotide	ORF	SEQ ID NO: Polypeptide
36	82-847	80
37	82-1104	81
38	0-1532	82
39	58-1632	83
40	0-1580	84
41	16-1596	85
42	0-1478	86
43	20-1519	87
44	117-1259	88

Once open reading frames are identified, the open reading frames may be isolated and/or synthesized. Expressible genetic constructs comprising the open reading frames and suitable promoters, initiators, terminators, etc., which are well known in the art, may then be constructed. Such genetic constructs may be introduced into a host cell to express the polypeptide encoded by the open reading frame. Suitable host cells may include various prokaryotic and eukaryotic cells, including plant cells, mammalian cells, bacterial cells, algae and the like.

The polynucleotides of the present invention may be isolated by high throughput sequencing of cDNA libraries prepared from forage grass tissue, as described below in Example 1. Alternatively, oligonucleotide probes and primers based on the sequences provided in SEQ ID NO: 1-44 can be synthesized as detailed below, and used to identify positive clones in either cDNA or genomic DNA libraries from forage grass tissue cells by means of hybridization or polymerase chain reaction (PCR) techniques. Hybridization and PCR techniques suitable for use with such oligonucleotide probes are well known in the art (see, for example, Mullis *et al.*, *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich, ed., *PCR technology*, Stockton Press: NY, 1989; and Sambrook *et al.*, eds., *Molecular cloning: a laboratory manual*, 2nd ed., CSHL Press: Cold Spring Harbor, NY, 1989). In addition to DNA-DNA hybridization, DNA-RNA or RNA-RNA hybridization assays are also possible. In the first case, the mRNA from expressed genes would then be detected instead of genomic DNA or cDNA derived from mRNA of the sample. In the second case, RNA probes could be used. Artificial analogs of DNA hybridizing specifically to target

sequences could also be employed. Positive clones may be analyzed by restriction enzyme digestion, DNA sequencing or the like.

The polynucleotides of the present invention may also, or alternatively, be synthesized using techniques that are well known in the art. The polynucleotides may be synthesized, for example, using automated oligonucleotide synthesizers (e.g., Beckman Oligo 1000M DNA Synthesizer; Beckman Coulter Ltd., Fullerton, CA) to obtain polynucleotide segments of up to 50 or more nucleic acids. A plurality of such polynucleotide segments may then be ligated using standard DNA manipulation techniques that are well known in the art of molecular biology. One conventional and exemplary polynucleotide synthesis technique involves synthesis of a single stranded polynucleotide segment having, for example, 80 nucleic acids, and hybridizing that segment to a synthesized complementary 85 nucleic acid segment to produce a 5 nucleotide overhang. The next segment may then be synthesized in a similar fashion, with a 5 nucleotide overhang on the opposite strand. The "sticky" ends ensure proper ligation when the two portions are hybridized. In this way, a complete polynucleotide of the present invention may be synthesized entirely *in vitro*.

Oligonucleotide probes and primers complementary to and/or corresponding to SEQ ID NO: 1-44 and variants of those sequences, are also comprehended by the present invention. Such oligonucleotide probes and primers are substantially complementary to the polynucleotide of interest over a certain portion of the polynucleotide. An oligonucleotide probe or primer is described as "corresponding to" a polynucleotide of the present invention, including one of the sequences set out as SEQ ID NO: 1-44 or a variant thereof, if the oligonucleotide probe or primer, or its complement, is contained within one of the sequences set out as SEQ ID NOS: 1-44 or a variant of one of the specified sequences.

Two single stranded sequences are said to be substantially complementary when the nucleotides of one strand, optimally aligned and compared, with the appropriate nucleotide insertions and/or deletions, pair with at least 80%, preferably at least 90% to 95%, and more preferably at least 98% to 100%, of the nucleotides of the other strand. Alternatively, substantial complementarity exists when a first DNA strand will selectively hybridize to a second DNA strand under stringent hybridization conditions.

In specific embodiments, the inventive oligonucleotide probes and/or primers comprise at least about 6 contiguous residues, more preferably at least about 10 contiguous

residues, and most preferably at least about 20 contiguous residues complementary to a polynucleotide sequence of the present invention. Probes and primers of the present invention may be from about 8 to 100 base pairs in length, preferably from about 10 to 50 base pairs in length, and more preferably from about 15 to 40 base pairs in length. The probes can be easily selected using procedures well known in the art, taking into account DNA-DNA hybridization stringencies, annealing and melting temperatures, potential for formation of loops, and other factors which are well known in the art. Preferred techniques for designing PCR primers are disclosed in Dieffenbach and Dykster, *PCR Primer: a laboratory manual*, CSHL Press: Cold Spring Harbor, NY, 1995. A software program suitable for designing probes, and especially for designing PCR primers, is available from Premier Biosoft International, 3786 Corina Way, Palo Alto, CA 94303-4504.

The isolated polynucleotides of the present invention also have utility in genome mapping, in physical mapping, and in positional cloning of genes.

The polynucleotides identified as SEQ ID NO: 1-44 were isolated from cDNA clones and represent sequences that are expressed in the tissue from which the cDNA was prepared. RNA sequences, reverse sequences, complementary sequences, anti-sense sequences, and the like, corresponding to the polynucleotides of the present invention, may be routinely ascertained and obtained using the cDNA sequences identified as SEQ ID NO: 1-44.

Identification of genomic DNA and heterologous species DNA can be accomplished by standard DNA/DNA hybridization techniques, under appropriately stringent conditions, using all or part of a polynucleotide sequence as a probe to screen an appropriate library. Alternatively, PCR techniques using oligonucleotide primers that are designed based on known genomic DNA, cDNA and protein sequences can be used to amplify and identify genomic and cDNA sequences.

In another aspect, the present invention provides isolated polypeptides encoded by the above polynucleotides. As used herein, the term "polypeptide" encompasses amino acid chains of any length, including full-length proteins, wherein the amino acid residues are linked by covalent peptide bonds. The term "polypeptide encoded by a polynucleotide" as used herein, includes polypeptides encoded by a polynucleotide that comprises a partial isolated polynucleotide sequence provided herein. In specific embodiments, the inventive



polypeptides comprise an amino acid sequence selected from the group consisting of SEQ ID NO: 45-88, as well as variants of such sequences.

As noted above, polypeptides of the present invention may be produced recombinantly by inserting a polynucleotide sequence encoding the polypeptide into an expression vector and expressing the polypeptide in an appropriate host. Any of a variety of expression vectors known to those of ordinary skill in the art may be employed. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a polynucleotide molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast, and higher eukaryotic cells. Preferably, the host cells employed are plant, *E. coli*, insect, yeast, or a mammalian cell line such as COS or CHO. The polynucleotide sequences expressed in this manner may encode naturally occurring polypeptides, portions of naturally occurring polypeptides, or other variants thereof. The expressed polypeptides may be used in various assays known in the art to determine their biological activity. Such polypeptides may also be used to raise antibodies, to isolate corresponding interacting proteins or other compounds, and to quantitatively determine levels of interacting proteins or other compounds.

In a related aspect, polypeptides are provided that comprise at least a functional portion of a polypeptide having an amino acid sequence selected from the group consisting of sequences provided in SEQ ID NO: 45-88 and variants thereof. As used herein, the “functional portion” of a polypeptide is that portion which contains an active site essential for affecting the function of the polypeptide, for example, a portion of the molecule that is capable of binding one or more reactants. The active site may be made up of separate portions present on one or more polypeptide chains and will generally exhibit high binding affinity. Functional portions of a polypeptide may be identified by first preparing fragments of the polypeptide by either chemical or enzymatic digestion of the polypeptide, or by mutation analysis of the polynucleotide that encodes the polypeptide and subsequent expression of the resulting mutant polypeptides. The polypeptide fragments or mutant polypeptides are then tested to determine which portions retain biological activity, using methods well known to those of skill in the art, including the representative assays described below.

Portions and other variants of the inventive polypeptides may be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85: 2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied Biosystems, Inc. (Foster City, California), and may be operated according to the manufacturer's instructions. Variants of a native polypeptide may be prepared using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (Kunkel, *Proc. Natl. Acad. Sci. USA* 82: 488-492, 1985). Sections of DNA sequences may also be removed using standard techniques to permit preparation of truncated polypeptides.

As used herein, the term "variant" comprehends nucleotide or amino acid sequences different from the specifically identified sequences, wherein one or more nucleotides or amino acid residues is deleted, substituted, or added. Variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant sequences (polynucleotide or polypeptide) preferably exhibit at least 75%, more preferably at least 80%, more preferably at least 90%, more preferably yet at least 95%, and most preferably at least 98% identity to a sequence of the present invention. The percentage identity is determined by aligning the two sequences to be compared as described below, determining the number of identical residues in the aligned portion, dividing that number by the total number of residues in the inventive (queried) sequence, and multiplying the result by 100.

Polynucleotides and polypeptides having a specified percentage identity to a polynucleotide or polypeptide identified in one of SEQ ID NO: 1-88 thus share a high degree of similarity in their primary structure. In addition to a specified percentage identity to a polynucleotide of the present invention, variant polynucleotides and polypeptides preferably have additional structural and/or functional features in common with a polynucleotide of the present invention. Polynucleotides having a specified degree of identity to, or capable of hybridizing to, a polynucleotide of the present invention preferably additionally have at least

one of the following features: (1) they contain an open reading frame, or partial open reading frame, encoding a polypeptide, or a functional portion of a polypeptide, having substantially the same functional properties as the polypeptide, or functional portion thereof, encoded by a polynucleotide in a recited SEQ ID NO.; or (2) they contain identifiable domains in common.

5 Polynucleotide or polypeptide sequences may be aligned, and percentages of identical nucleotides or amino acids in a specified region may be determined against another polynucleotide or polypeptide, using computer algorithms that are publicly available. For example, the BLASTN and FASTA algorithms, set to the default parameters described in the documentation and distributed with the algorithm, may be used for aligning and identifying  
10 the similarity of polynucleotide sequences. The alignment and similarity of polypeptide sequences may be examined using the BLASTP algorithm. BLASTX and FASTX algorithms compare nucleotide query sequences translated in all reading frames against polypeptide sequences. The FASTA and FASTX algorithms are described in Pearson and Lipman, *Proc. Natl. Acad. Sci. USA* 85:2444-2448, 1988; and in Pearson, *Methods in*  
15 *Enzymol.* 183:63-98, 1990. The FASTA software package is available from the University of Virginia by contacting the Assistant Provost for Research, University of Virginia, PO Box 9025, Charlottesville, VA 22906-9025. The BLASTN software is available from the National Center for Biotechnology Information (NCBI), National Library of Medicine, Building 38A, Room 8N805, Bethesda, MD 20894. The BLASTN algorithm Version 2.0.11  
20 [Jan-20-2000] set to the default parameters described in the documentation and distributed with the algorithm, is preferred for use in the determination of polynucleotide variants according to the present invention. The use of the BLAST family of algorithms, including BLASTN, BLASTP and BLASTX, is described in the publication of Altschul *et al.*, "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs," *Nucleic*  
25 *Acids Res.* 25:3389-3402, 1997.

The following running parameters are preferred for determination of alignments and similarities using BLASTN that contribute to the percentage identity and E values for polynucleotides: Unix running command with the following default parameters: blastall -p  
blastn -d embldb -e 10 -G 0 -E 0 -r 1 -v 30 -b 30 -i queryseq -o results; and parameters are:  
30 -p Program Name [String]; -d Database [String]; -e Expectation value (E) [Real]; -G Cost to open a gap (zero invokes default behavior) [Integer]; -FF low complexity filter; -E Cost to

extend a gap (zero invokes default behavior) [Integer]; -r Reward for a nucleotide match (BLASTN only) [Integer]; -v Number of one-line descriptions (V) [Integer]; -b Number of alignments to show (B) [Integer]; -i Query File [File In]; -o BLAST report Output File [File Out] Optional.

- 5           The following running parameters are preferred for determination of alignments and similarities using BLASTP that contribute to the percentage identity and E values of polypeptide sequences: blastall -p blastp -d swissprotodb -e 10 -G 0 -E 0 -FF -v 30 -b 30 -i queryseq -o results; the parameters are: -p Program Name [String]; -d Database [String]; -e Expectation value (E) [Real]; -G Cost to open a gap (zero invokes default behavior)
- 10 [Integer]; -FF low complexity filter; -E Cost to extend a gap (zero invokes default behavior) [Integer]; -v Number of one-line descriptions (v) [Integer]; -b Number of alignments to show (b) [Integer]; -I Query File [File In]; -o BLAST report Output File [File Out] Optional.

- The "hits" to one or more database sequences by a queried sequence produced by BLASTN, BLASTP, FASTA or a similar algorithm, align and identify similar portions of
- 15 sequences. The hits are arranged in order of the degree of similarity and the length of sequence overlap. Hits to a database sequence generally represent an overlap over only a fraction of the sequence length of the queried sequence.

- As noted above, the percentage identity of a polynucleotide or polypeptide sequence is determined by aligning polynucleotide and polypeptide sequences using appropriate
- 20 algorithms, such as BLASTN or BLASTP, respectively, set to default parameters; identifying the number of identical nucleic or amino acids over the aligned portions; dividing the number of identical nucleic or amino acids by the total number of nucleic or amino acids of the polynucleotide or polypeptide of the present invention; and then multiplying by 100 to determine the percentage identity. By way of example, a queried polynucleotide having 220
- 25 nucleic acids has a hit to a polynucleotide sequence in the EMBL database having 520 nucleic acids over a stretch of 23 nucleotides in the alignment produced by the BLASTN algorithm using the default parameters. The 23-nucleotide hit includes 21 identical nucleotides, one gap and one different nucleotide. The percentage identity of the queried polynucleotide to the hit in the EMBL database is thus 21/220 times 100, or 9.5%. The
- 30 percentage identity of polypeptide sequences may be determined in a similar fashion.

The BLASTN and BLASTX algorithms also produce "Expect" values for polynucleotide and polypeptide alignments. The Expect value (E) indicates the number of hits one can "expect" to see over a certain number of contiguous sequences by chance when searching a database of a certain size. The Expect value is used as a significance threshold for determining whether the hit to a database indicates true similarity. For example, an E value of 0.1 assigned to a polynucleotide hit is interpreted as meaning that in a database of the size of the EMBL database, one might expect to see 0.1 matches over the aligned portion of the sequence with a similar score simply by chance. By this criterion, the aligned and matched portions of the sequences then have a probability of 90% of being related. For sequences having an E value of 0.01 or less over aligned and matched portions, the probability of finding a match by chance in the EMBL database is 1% or less using the BLASTN algorithm. E values for polypeptide sequences may be determined in a similar fashion using various polypeptide databases, such as the SwissProt database.

According to one embodiment, "variant" polynucleotides and polypeptides, with reference to each of the polynucleotides and polypeptides of the present invention, preferably comprise sequences having the same number or fewer nucleotides or amino acids than each of the polynucleotides or polypeptides of the present invention and producing an E value of 0.01 or less when compared to the polynucleotide or polypeptide of the present invention. That is, a variant polynucleotide or polypeptide is any sequence that has at least a 99% probability of being related to the polynucleotide or polypeptide of the present invention, measured as having an E value of 0.01 or less using the BLASTN or BLASTX algorithms set at the default parameters. According to a preferred embodiment, a variant polynucleotide is a sequence having the same number or fewer nucleic acids than a polynucleotide of the present invention that has at least a 99% probability of being related to the polynucleotide of the present invention, measured as having an E value of 0.01 or less using the BLASTN algorithm set at the default parameters. Similarly, according to a preferred embodiment, a variant polypeptide is a sequence having the same number or fewer amino acids than a polypeptide of the present invention that has at least a 99% probability of being related as the polypeptide of the present invention, measured as having an E value of 0.01 or less using the BLASTP algorithm set at the default parameters.

In an alternative embodiment, variant polynucleotides are sequences that hybridize to a polynucleotide of the present invention under stringent conditions. Stringent hybridization conditions for determining complementarity include salt conditions of less than about 1 M, more usually less than about 500 mM, and preferably less than about 200 mM. Hybridization temperatures can be as low as 5°C, but are generally greater than about 22°C, more preferably greater than about 30°C, and most preferably greater than about 37°C. Longer DNA fragments may require higher hybridization temperatures for specific hybridization. Since the stringency of hybridization may be affected by other factors such as probe composition, presence of organic solvents, and extent of base mismatching, the combination of parameters is more important than the absolute measure of any one alone. An example of "stringent conditions" is prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65°C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65°C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65°C.

The present invention also encompasses polynucleotides that differ from the disclosed sequences but that, as a consequence of the discrepancy of the genetic code, encode a polypeptide having similar enzymatic activity to a polypeptide encoded by a polynucleotide of the present invention. Thus, polynucleotides comprising sequences that differ from the polynucleotide sequences recited in SEQ ID NO: 1-44, or complements, reverse sequences, or reverse complements of those sequences, as a result of conservative substitutions are contemplated by and encompassed within the present invention. Additionally, polynucleotides comprising sequences that differ from the polynucleotide sequences recited in SEQ ID NO: 1-44, or complements, reverse complements or reverse sequences thereof, as a result of deletions and/or insertions totaling less than 10% of the total sequence length are also contemplated by and encompassed within the present invention. Similarly, polypeptides comprising sequences that differ from the polypeptide sequences recited in SEQ ID NO: 45-88 as a result of amino acid substitutions, insertions, and/or deletions totaling less than 10% of the total sequence length are contemplated by and encompassed within the present invention, provided the variant polypeptide has activity in a fructan, cellulose, starch and/or tannin biosynthetic pathway.

In another aspect, the present invention provides genetic constructs comprising, in the 5'-3' direction, a gene promoter sequence; an open reading frame coding for at least a functional portion of a polypeptide of the present invention; and a gene termination sequence. The open reading frame may be orientated in either a sense or anti-sense direction. For applications where amplification of fructan, cellulose, starch or tannin synthesis is desired, the open reading frame may be inserted in the construct in a sense orientation, such that transformation of a target organism with the construct will lead to an increase in the number of copies of the gene and therefore an increase in the amount of enzyme. When down-regulation of fructan, cellulose, starch or tannin synthesis is desired, the open reading frame may be inserted in the construct in an anti-sense orientation, such that the RNA produced by transcription of the polynucleotide is complementary to the endogenous mRNA sequence. This, in turn, will result in a decrease in the number of copies of the gene and therefore a decrease in the amount of enzyme. Alternatively, regulation may be achieved by inserting appropriate sequences or subsequences (*e.g.*, DNA or RNA) in ribozyme constructs.

Genetic constructs comprising a non-coding region of a gene coding for a polypeptide of the present invention, or a nucleotide sequence complementary to a non-coding region, together with a gene promoter sequence and a gene termination sequence, are also provided. As used herein the term "non-coding region" includes both transcribed sequences which are not translated, and non-transcribed sequences within about 2000 base pairs 5' or 3' of the translated sequences or open reading frames. Examples of non-coding regions which may be usefully employed in the inventive constructs include introns and 5'-non-coding leader sequences. Transformation of a target plant with such a genetic construct may lead to a reduction in the amount of fructan, cellulose, starch or tannin synthesized by the plant by the process of cosuppression, in a manner similar to that discussed, for example, by Napoli *et al.*, *Plant Cell* 2:279-290, 1990; and de Carvalho Niebel *et al.*, *Plant Cell* 7:347-358, 1995.

The genetic constructs of the present invention further comprise a gene promoter sequence and a gene termination sequence, operably linked to the polynucleotide to be transcribed, which control expression of the gene. The gene promoter sequence is generally positioned at the 5' end of the polynucleotide to be transcribed, and is employed to initiate transcription of the polynucleotide. Gene promoter sequences are generally found in the 5' non-coding region of a gene but they may exist in introns (Luehrsen, *Mol. Gen. Genet.*

225:81-93, 1991) or in the coding region, as for example in PAL of tomato (Bloksberg, *Studies on the Biology of Phenylalanine Ammonia Lyase and Plant Pathogen Interaction*, Ph.D. Thesis, University of California, Davis, 1991, University Microfilms International Order No. 9217564). When the construct includes an open reading frame in a sense orientation, the gene promoter sequence also initiates translation of the open reading frame. For genetic constructs comprising either an open reading frame in an anti-sense orientation or a non-coding region, the gene promoter sequence consists only of a transcription initiation site having a RNA polymerase binding site.

A variety of gene promoter sequences which may be usefully employed in the genetic constructs of the present invention are well known in the art. The promoter gene sequence, and also the gene termination sequence, may be endogenous to the target plant host or may be exogenous, provided the promoter is functional in the target host. For example, the promoter and termination sequences may be from other plant species, plant viruses, bacterial plasmids and the like. Preferably, gene promoter and termination sequences are from the inventive sequences themselves.

Factors influencing the choice of promoter include the desired tissue specificity of the construct, and the timing of transcription and translation. For example, constitutive promoters, such as the 35S Cauliflower Mosaic Virus (CaMV 35S) promoter or the superubiquitin promoter (PCT International Patent Publication WO 00/58474), will affect the activity of the enzyme in all parts of the plant. Use of a tissue specific promoter will result in production of the desired sense or anti-sense RNA only in the tissue of interest. With DNA constructs employing inducible gene promoter sequences, the rate of RNA polymerase binding and initiation can be modulated by external stimuli, such as light, heat, anaerobic stress, alteration in nutrient conditions and the like. Temporally regulated promoters can be employed to effect modulation of the rate of RNA polymerase binding and initiation at a specific time during development of a transformed cell. Preferably, the original promoters from the enzyme gene in question, or promoters from a specific tissue-targeted gene in the organism to be transformed, such as *Lolium* or *Festuca*, are used. Grass promoters different from the original gene may also be usefully employed in the inventive genetic constructs in order to prevent feedback inhibition. For example, the fructosyltransferase gene will be regulated by sucrose sensing systems; therefore removing the gene from under control of its



normal promoter allows the gene to be active all the time. Other examples of gene promoters which may be usefully employed in the present invention include, mannopine synthase (mas), octopine synthase (ocs) and those reviewed by Chua *et al.*, *Science* 244:174-181, 1989.

5       The gene termination sequence, which is located 3' to the polynucleotide to be transcribed, may come from the same gene as the gene promoter sequence or may be from a different gene. Many gene termination sequences known in the art may be usefully employed in the present invention, such as the 3' end of the *Agrobacterium tumefaciens* nopaline synthase gene. However, preferred gene terminator sequences are those from the  
10       original enzyme gene or from the target species to be transformed.

      The genetic constructs of the present invention may also contain a selection marker that is effective in plant cells, to allow for the detection of transformed cells containing the inventive construct. Such markers, which are well known in the art, typically confer resistance to one or more toxins. One example of such a marker is the NPTII gene whose  
15       expression results in resistance to kanamycin or hygromycin, antibiotics which are usually toxic to plant cells at a moderate concentration (Rogers *et al.*, in Weissbach A and H, eds., *Methods for Plant Molecular Biology*, Academic Press Inc.: San Diego, CA, 1988). Alternatively, the presence of the desired construct in transformed cells can be determined by means of other techniques well known in the art, such as Southern and Western blots.

20       Techniques for operatively linking the components of the inventive genetic constructs are well known in the art and include the use of synthetic linkers containing one or more restriction endonuclease sites as described, for example, by Sambrook *et al.*, (*Molecular cloning: a laboratory manual*, CSHL Press: Cold Spring Harbor, NY, 1989). The genetic construct of the present invention may be linked to a vector having at least one replication  
25       system, for example, *E. coli*, whereby after each manipulation, the resulting construct can be cloned and sequenced, and the correctness of the manipulation determined.

      The genetic constructs of the present invention may be used to transform a variety of plants, both monocotyledonous (*e.g.*, grasses, maize/corn, grains, oats, rice, sorghum, millet, rye, sugar cane, wheat and barley), dicotyledonous (*e.g.*, *Arabidopsis*, tobacco, legumes,  
30       alfalfa, oaks, eucalyptus, maple), and gymnosperms. In a preferred embodiment, the inventive genetic constructs are employed to transform grasses. Preferably the target plant is

selected from the group consisting of *Lolium* and *Festuca* species, most preferably from the group consisting of *Lolium perenne* and *Festuca arundinacea*. Plants that may be usefully transformed with the inventive genetic constructs include other species of ryegrass and fescue, including, but not limited to *Lolium multiflorum* (Italian ryegrass), *Lolium hybridum* 5 (hybrid ryegrass), *Lolium rigidum* (Wimmera grass), *Lolium temulentum* (darnel), *Festuca rubra* (red fescue) and *Festuca pratensis* (meadow fescue). As discussed above, transformation of a plant with a genetic construct of the present invention will produce a modified fructan, cellulose, starch or tannin content in the plant.

The production of RNA in target cells may be controlled by choice of the promoter 10 sequence, or by selecting the number of functional copies or the site of integration of the polynucleotides incorporated into the genome of the target organism. A target plant may be transformed with more than one construct of the present invention, thereby modulating the fructan, cellulose, starch and/or tannin biosynthetic pathways by affecting the activity of more than one enzyme, affecting enzyme activity in more than one tissue, or affecting 15 enzyme activity at more than one expression time. Similarly, a construct may be assembled containing more than one open reading frame coding for an enzyme encoded by a polynucleotide of the present invention or more than one non-coding region of a gene coding for such an enzyme. The polynucleotides of the present invention may also be employed in combination with other known sequences encoding enzymes involved in the lignin, fructan 20 and/or tannin biosynthetic pathways. In this manner, more than one biosynthetic pathway may be modulated, or a fructan, cellulose, starch or tannin biosynthetic pathway may be added to a plant to produce a plant having an altered phenotype.

Techniques for stably incorporating genetic constructs into the genome of target plants are well known in the art and include *Agrobacterium tumefaciens* mediated 25 introduction, electroporation, protoplast fusion, injection into reproductive organs, injection into immature embryos, high velocity projectile introduction and the like. The choice of technique will depend upon the target plant to be transformed. For example, dicotyledonous plants, and certain monocots and gymnosperms may be transformed by *Agrobacterium* Ti plasmid technology, as described, for example by Bevan, *Nucleic Acid Res.* 12:8711-8721, 30 1984. Targets for the introduction of the genetic constructs of the present invention include tissues, such as leaf tissue, disseminated cells, protoplasts, seeds, embryos, meristematic

regions; cotyledons, hypocotyls, and the like. Transformation techniques which may be usefully employed in the inventive methods include those taught by Ellis *et al.*, *Plant Cell Reports*, 8:16-20, 1989; Wilson *et al.*, *Plant Cell Reports* 7:704-707, 1989; and Tautorus *et al.*, *Theor. Appl. Genet.* 78:531-536, 1989.

5           Once the cells are transformed, cells having the inventive genetic construct incorporated in their genome may be selected by means of a marker, such as the kanamycin resistance marker discussed above. Transgenic cells may then be cultured in an appropriate medium to regenerate whole plants, using techniques well known in the art. In the case of protoplasts, the cell wall is allowed to reform under appropriate osmotic conditions. In the  
10 case of seeds or embryos, an appropriate germination or callus initiation medium is employed. For explants, an appropriate regeneration medium is used. Regeneration of plants is well established for many species. The resulting transformed plants may be reproduced sexually or asexually, using methods well known in the art, to give successive generations of transgenic plants.

15           Polynucleotides of the present invention may also be used to specifically suppress gene expression by methods that operate post-transcriptionally to block the synthesis of products of targeted genes, such as RNA interference (RNAi), and quelling. Briefly, traditional methods of gene suppression, employing anti-sense RNA or DNA, operate by binding to the reverse sequence of a gene of interest such that binding interferes with  
20 subsequent cellular processes and therefore blocks synthesis of the corresponding protein. RNAi also operates on a post-translational level and is sequence specific, but suppresses gene expression far more efficiently. Exemplary methods for controlling or modifying gene expression using RNAi are provided in US Patent 6,506,559 and PCT International Publications WO 99/49029 and WO 99/53050. In these methods, post-transcriptional gene  
25 silencing is brought about by a sequence-specific RNA degradation process which results in the rapid degradation of transcripts of sequence-related genes. Studies have shown that double-stranded RNA may act as a mediator of sequence-specific gene silencing (see, for example, Montgomery and Fire, *Trends in Genetics*, 14:255-258, 1998). Gene constructs that produce transcripts with self-complementary regions are particularly efficient at gene  
30 silencing. A unique feature of this post-transcriptional gene silencing pathway is that silencing is not limited to the cells where it is initiated. The gene-silencing effects may be

disseminated to other parts of an organism and even transmitted through the germ line to several generations.

5 The polynucleotides of the present invention may thus be employed to generate gene silencing constructs and/or gene-specific self-complementary RNA sequences that can be delivered by conventional art-known methods to plant tissues, such as forage grass tissues. Within genetic constructs, sense and antisense sequences can be placed in regions flanking an intron sequence in proper splicing orientation with donor and acceptor splicing sites, such that intron sequences are removed during processing of the transcript, and sense and antisense sequences, as well as splice junction sequences, bind together to form double-  
10 stranded RNA. Alternatively, spacer sequences of various lengths may be employed to separate self-complementary regions of sequence in the construct. During processing of the gene construct transcript, intron sequences are spliced-out, allowing sense and anti-sense sequences, as well as splice junction sequences, to bind forming double-stranded RNA. Select ribonucleases then bind to and cleave the double-stranded RNA, thereby initiating the  
15 cascade of events leading to degradation of specific mRNA gene sequences, and silencing specific genes. Alternatively, rather than using a gene construct to express the self-complementary RNA sequences, the gene-specific double-stranded RNA segments are delivered to one or more targeted areas to be internalized into the cell cytoplasm to exert a gene silencing effect. The double-stranded RNA must have sufficient homology to the  
20 targeted gene to mediate RNAi and is preferably at least 25 nucleotides in length. Preferably, the double-stranded RNA corresponds specifically to a polynucleotide of the present invention. Gene silencing RNA sequences comprising the polynucleotides of the present invention are useful for creating genetically modified plants with desired phenotypes as well as for characterizing genes (for example, in high-throughput screening of sequences), and  
25 studying their functions in intact organisms.

Example 1ISOLATION OF cDNA SEQUENCES FROM *L. PERENNE* AND  
*F. ARUNDINACEA* cDNA LIBRARIES

5        *L. perenne* and *F. arundinacea* cDNA expression libraries were constructed and screened as follows. Tissue was collected from *L. perenne* and *F. arundinacea* during winter and spring, and snap-frozen in liquid nitrogen. The tissues collected included those obtained from leaves, pseudostem, roots, inflorescence (day 0), stem bases from day 7 emerged inflorescence, basal leaf day 3 and day 6, floral stem and vegetative stem. Total RNA was isolated from each tissue type using TRIzol Reagent (BRL Life Technologies, Gaithersburg, MD). mRNA from each tissue type was obtained using a Poly(A) Quik mRNA isolation kit (Stratagene, La Jolla, CA), according to the manufacturer's specifications. cDNA expression libraries were constructed from the purified mRNA by reverse transcriptase synthesis followed by insertion of the resulting cDNA in Lambda ZAP using a ZAP Express cDNA Synthesis Kit (Stratagene), according to the manufacturer's protocol. The resulting cDNA clones were packaged using a Gigapack II Packaging Extract (Stratagene) employing 1 µl of sample DNA from the 5 µl ligation mix. Mass excision of the libraries was performed using XL1-Blue MRF' cells and XL0LR cells (Stratagene) with ExAssist helper phage (Stratagene). The excised phagemids were diluted with NZY broth (Gibco BRL, Gaithersburg, MD) and plated out onto LB-kanamycin agar plates containing 5-bromo-4-chloro-3-indolyl-beta-D-galactosidase (X-gal) and isopropylthio-beta-galactoside (IPTG).

20        Of the colonies plated and picked for DNA preparations, the large majority contained an insert suitable for sequencing. Positive colonies were cultured in NZY broth with kanamycin and DNA was purified following standard protocols. Agarose gel at 1% was used to screen sequencing templates for chromosomal contamination. Dye terminator sequences were prepared using a Biomek 2000 robot (Beckman Coulter Inc., Fullerton, CA) for liquid handling and DNA amplification using a 9700 PCR machine (Perkin Elmer/Applied Biosystems, Foster City, CA) according to the manufacturer's protocol.

25        The DNA sequences for positive clones were obtained using a Perkin Elmer/Applied Biosystems Division Prism 377 sequencer. cDNA clones were sequenced from the 5' end. The polynucleotide sequences identified as SEQ ID NO: 1, 3-5, 8-15, 17, 18, 20, 25, 27, 28,

30, 36-39 and 44 were identified from *Lolium perenne* cDNA expression libraries, with the polynucleotides of SEQ ID NO: 2, 6, 7, 16, 19, 21-24, 26, 29, 31-35 and 40-43 being identified from *Festuca arundinacea* cDNA expression libraries.

#### 5 BLASTN Polynucleotide Analysis

The isolated cDNA sequences were compared to sequences in the EMBL DNA database using the computer algorithm BLASTN. Comparisons of DNA sequences provided in SEQ ID NO: 1-44 to sequences in the EMBL DNA database were made as of April 28, 2003, using BLASTN algorithm Version 2.0.11 [Jan-20-2000], and the following Unix  
10 running command: blastall -p blastn -d embldb -e 10 -FF -G0 -E0 -r 1 -v 30 -b 30 -i queryseq -o.

The sequences of SEQ ID NO: 6-9, 11-19, 21, 25-27 and 34-44 were determined to have less than 50% identity, determined as described above using the computer algorithm BLASTN, to sequences in the EMBL database. The sequence of SEQ ID NO: 3, 4, 10, 20,  
15 22-24, 28, 29 and 31-33 was determined to have less than 75% identity, determined as described above, to sequences in the EMBL database, using the computer algorithm BLASTN, as described above. The sequences of SEQ ID NO: 1, 2 and 30 were determined to have less than 90% identity to sequences in the EMBL database using the computer algorithm BLASTN, as described above. Finally, the sequence of SEQ ID NO: 5 were  
20 determined to have less than 98% identity to sequences in the EMBL database using the computer algorithm BLASTN, as described above.

#### BLASTP Polypeptide Analysis

The isolated sequences were compared to sequences in the SwissProt protein database  
25 using the computer algorithm BLASTP. Specifically, comparisons of polypeptide sequences provided in SEQ ID NO: 45-88 to sequences in the SwissProt protein database were made as of April 28, 2003, using BLASTP algorithm Version 2.0.11 [Jan-20-2000], and the following Unix running command: blastall -p blastp -d swissprotodb -e 10 -FF -G0 -E0 -v 30 -b 30 -i queryseq -o.

30 The sequences of SEQ ID NO: 78-81 were determined to have less than 50% identity to sequences in the SwissProt database using the computer algorithm BLASTP as described

above. The sequences of SEQ ID NO: 51, 53, 55, 56, 71, 83 and 88 were determined to have less than 75% identity to sequences in the SwissProt database using the computer algorithm BLASTP, as described above. The sequences of SEQ ID NO: 50, 52, 54, 57-68, 82 and 84-87 were determined to have less than 90% identity to sequences in the SwissProt database using the computer algorithm BLASTP, as described above. Finally, the sequences of SEQ ID NO: 45-49, 69, 70 and 72-77 were determined to have less than 98% identity to sequences in the SwissProt database using the computer algorithm BLASTP, as described above.

#### 10 BLASTX Polynucleotide Analysis

The isolated cDNA sequences were compared to sequences in the SwissProt protein database using the computer algorithm BLASTX. Comparisons of DNA sequences provided in SEQ ID NOS: 1-44, to sequences in the SwissProt DNA database (using BLASTX) were made as of April 28, 2003, using BLAST algorithm Version 2.0.11 [Jan-20-2000], and the following Unix running command: blastall -p blastx -d swissprotodb -e 10 -FF -G0 -E0 -r 1 -v 30 -b 30 -i queryseq -o.

The sequences of SEQ ID NO: 27 and 34-37 were determined to have less than 50% identity, determined as described above, to sequences in the SwissProt database using the computer algorithm BLASTX, as described above. The sequences of SEQ ID NO: 3, 4, 6-19, 21-26, 28, 29, 33 and 38-44 were determined to have less than 75% identity, determined as described above, to sequences in the SwissProt database using the computer algorithm BLASTX, as described above. Finally, the sequences of SEQ ID NO: 1, 2, 5, 20 and 30-32 were determined to have less than 90% identity, determined as described above, to sequences in the SwissProt database using the computer algorithm BLASTX, as described above.

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Figs. 3-41 show the positions of domains within the amino acid sequences of SEQ ID NO: 45-48, 53-70 and 72-88, respectively. These domains were determined with InterProScan software Release v3.1, November 6, 2001. The InterPro database integrates PROSITE, PRINTS, Pfam, ProDom, SMART and TIGRFAMs databases, and the addition of others is scheduled. InterPro data is distributed in XML format and it is freely available under the InterPro Consortium copyright. The European Bioinformatics Institute (EBI) is a

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non-profit academic organization that forms part of the European Molecular Biology Laboratory (EMBL): Wellcome Trust Genome Campus, Hinxton, Cambridge, CB10 1SD UK.

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### Example 2

#### USE OF CHALCONE SYNTHASE GENES TO MODIFY TANNIN BIOSYNTHESIS

Certain *Arabidopsis* mutants of the *transparent testa* (*tt*) phenotype do not make the anthocyanin pigment cyanidin and therefore have no seed coat color. The genes responsible for many of these mutants have now been identified as shown in Table 3.

**TABLE 3**

Enzyme	Abbreviation	Locus	Chromosome
Dihydroflavanol-4-reductase	DFR	<i>tt3</i>	5
Chalcone synthase	CHS	<i>tt4</i>	5
Chalcone isomerase	CHI	<i>tt5</i>	3
Flavanone 3- $\beta$ -hydroxylase	F3 $\beta$ H	<i>tt6</i>	3

15

Over-expression of the maize gene for CHS has been shown to complement the *Arabidopsis tt4* mutant, thereby restoring cyanidin synthesis and seed coat color (Dong *et al.*, *Plant Physiol.* 127:46-57, 2001). Complementation of these *Arabidopsis* mutants may therefore be employed to demonstrate the function of the inventive polynucleotides encoding enzymes involved in the tannin biosynthetic pathway.

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Two chalcone synthase genes were identified from *F. arundinacea* (SEQ ID NO: 32 and 33). Sense constructs containing a polynucleotide including the coding region of one chalcone synthase gene, FaCHS2, (SEQ ID NO: 33) under the control of the CaMV 35S promoter were inserted into a binary vector and used to transform *Agrobacterium tumefaciens* LBA4404 using published methods (*see*, An G, Ebert PR, Mitra A, Ha SB, "Binary Vectors," in Gelvin SB, Schilperoort RA, eds., *Plant Molecular Biology Manual*, Kluwer Academic Publishers: Dordrecht, 1988). The presence and integrity of the binary

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vector in *A. tumefaciens* was verified by polymerase chain reaction (PCR) using the forward primer provided in SEQ ID NO: 89 and reverse primer provided in SEQ ID: 90.

The *A. tumefaciens* containing the sense gene construct were used to transform *Arabidopsis tt4* mutants by floral dipping (Clough and Bent, *Plant J.* 16:735-743, 1998) and several independent transformed plant lines were established for the sense. Transformed plants containing the appropriate tannin gene construct were verified using PCR.

The presence of cyanidin in the transformed plants is demonstrated by a phenotypic change in plant seedling color and by analyzing cyanidin extracts made from transgenic plants grown under stressed conditions (Dong *et al.*, *Plant Physiol.* 127:46-57, 2001).

Briefly, cyanidins are extracted from plant tissue with an acid/alcohol solution (HCl/methanol) and water. Chlorophyll is removed by freezing the extracts followed by centrifugation at 4 °C at 20,000 x g for 20 min. Any remaining chlorophyll is removed through a chloroform extraction. The absorbance at 530 nm is measured for each of the cyanidin extracts. Non-transgenic wild type and control *Arabidopsis* plants are used as controls.

### Example 3

#### USE OF SUCROSE TRANSPORTERS TO COMPLEMENT A YEAST STRAIN

##### UNABLE TO GROW ON SUCROSE

Two *Lolium perenne* genes, LpSUT2 (SEQ ID: 25) and LpSUT-like (SEQ ID: 27), and two *Festuca arundinacea* genes, FaSUT1 (SEQ ID NO: 22) and FaSUT2 (SEQ ID NO: 26) share amino acid sequence identity with sucrose transporter (SUT1 and SUT2) genes from other plant species (Barker *et al.*, *Plant Cell* 12:1153-1164, 2000; Weise *et al.*, *Plant Cell* 12:1345-1355, 2000; Lemoine, *Biochim. Biophys. Acta* 1465:246-262, 2000). The first plant gene encoding a sucrose carrier protein, from spinach, was isolated by functional expression in a yeast strain, SUSY7 (Riesmeier *et al.*, *EMBO J.* 11:4705-4713, 1992).

The gene of SEQ ID NO: 27 was digested and cloned into the yeast expression vector pYEP 112 A1 NE for functional complementation using this yeast system. Plasmid DNA was verified by sequencing and transformed into *S. cerevisiae* strain SUSY7, which had been

engineered to express cytosolic sucrose synthase enabling it to metabolize sucrose entering the cell. Constitutive expression of the grass sucrose transporters within this yeast strain facilitated transport of sucrose in to the cell and its growth on sucrose minimal media. Growth rates of recombinant and wild type yeast strains in both sucrose and glucose minimal media were observed.

Results showed that the yeast strain containing the gene of SEQ ID NO: 27 was able to grow on sucrose minimal medium because the constitutive expression of the SUT-like gene within this yeast strain facilitated transport of sucrose into the cell.

#### Example 4

##### USE OF ALKALINE/NEUTRAL INVERTASES TO CLEAVE SUCROSE

A number of *Lolium perenne* and *Festuca arundinacea* genes (SEQ ID NO: 5, 7 and 9-14) were identified that share amino acid sequence identity with alkaline/neutral invertase genes from other plant species (Sturm *et al.*, *Physiol. Planta* 107:159-165, 1999; Gallagher and Pollock, *J. Exp. Bot.* 49:789-795, 1998).

*L. perenne* gene AN\_INV8 (SEQ ID NO: 12) was amplified by PCR from the start methionine using forward (SEQ ID NO: 91) and reverse (SEQ ID NO: 92) primers, then cloned into the pET41a expression plasmid. The resulting plasmid was transformed into *E. coli* BL21 cells using standard protocols, and protein expression induced using IPTG. The soluble recombinant protein was assayed for its ability to cleave sucrose. Cells were lysed in citrate buffer and the soluble protein incubated with 50mM sucrose in citrate buffer pH7. Reactions were terminated by boiling. Cleavage of the sucrose by neutral invertase activity was determined by the formation of glucose in this reaction. Levels of glucose were determined with a Glucose HK assay kit GAHK-20 (Sigma, St Louis MO) utilizing hexokinase coupled to glucose-6-phosphate dehydrogenase, and reduction of NAD measured by absorbance at 340nm.

Fig. 1 shows the invertase activity of recombinant AN\_INV8 protein, measured as the amount (in  $\mu$ g) of glucose release from cleavage of sucrose per hour at pH7, and that of an empty vector (pET41a) control sample. The results showed that the purified protein released

35  $\mu$ g of glucose per hour through the invertase cleavage of sucrose. . No release was measured with the empty vector control.

### Example 5

5 USE OF PYROPHOSPHATE-DEPENDENT PHOSPHOFRUCTOKINASE TO PHOSPHORYLATE  
FRUCTOSE-6-PHOSPHATE

Two *Lolium perenne* genes, LpPFPA (SEQ ID: 15) and LpPFPB (SEQ ID NO: 18), and two *Festuca arundinacea* genes, FaPFPA (SEQ ID NO: 16) and FaPFPB (SEQ ID NO: 19) share amino acid sequence identity with the A and B subunits of pyrophosphate-dependent phosphofructoskinase genes (PFP) from other plant species (Todd *et al.*, *Gene* 152:181-186, 1995; Carlisle *et al.*, *J. Biol. Chem.* 265:18366-18371, 1990).

The entire coding regions were cloned into expression vector pBK-CMV, under the control of the CMV promoter for expression of recombinant protein in mammalian cells. The PFPA and PFPB genes from *Lolium perenne* or *Festuca arundinacea* were co-transfected in to mammalian HEK293T cells and protein extracted 48 hours later. Protein was also extracted from cells transfected with a negative control vector containing the  $\beta$ -galactosidase gene. Purified potato PFP (Sigma, St. Louis MO) was used as positive control. Activity of the PFP enzyme was measured spectrophotometrically by a decrease NADH and absorbance at 340 nm in a coupled reaction as described previously (Theodorou and Kruger, *Planta* 213:147-157, 2001). Briefly, the conversion of fructose-6-phosphate to fructose-1,6-diphosphate in the presence of activator, fructose-2,6-diphosphate was initiated by the addition of pyrophosphate and measured in a coupled reaction with aldolase, triose phosphate isomerase and glycerophosphate dehydrogenase.

Fig. 2 shows the PFP activity of the purified protein (conversion of fructose-6-phosphate to fructose-1-6-diphosphate) measured as conversion of PPi to inorganic phosphate. No conversion was obtained with the  $\beta$ -galactosidase negative control.

Example 6USE OF SUCROSE PHOSPHATE SYNTHASE ENZYMES TO SYNTHESIZE SUCROSE

A *Lolium perenne* polynucleotide sequence (SEQ ID NO: 20) and a *F. arundinacea* polynucleotide sequence (SEQ ID NO: 21) have been identified that share identity with sucrose phosphate synthase (SPS) from other plant species. These genes are expressed in *E. coli* or *Pichia* using standard protocols, and the resulting purified protein assayed for its ability to synthesize sucrose from fructose-6-phosphate and uridine 5'-diphosphoglucose. Sucrose is detected by adding NAD and UDP-Glucose dehydrogenase, followed by the addition of anthrone reagent and then measuring the change in absorbance at 620 nm (Botha and Black, *Aust. J. Plant Physiol.* 27:81-85, 2000).

SEQ ID NOS: 1-88 are set out in the attached Sequence Listing. The codes for nucleotide sequences used in the attached Sequence Listing, including the symbol "n," conform to WIPO Standard ST.25 (1998), Appendix 2, Table 1.

All references cited herein, including patent references and non-patent publications, are hereby incorporated by reference in their entireties.

While in the foregoing specification this invention has been described in relation to certain preferred embodiments, and many details have been set forth for purposes of illustration, it will be apparent to those skilled in the art that the invention is susceptible to additional embodiments and that certain of the details described herein may be varied considerably without departing from the basic principles of the invention.

Claims

We claim:

1. An isolated polynucleotide comprising a sequence selected from the group consisting  
5 of: SEQ ID NO: 1-44.
2. An isolated polynucleotide comprising a sequence selected from the group consisting  
of:
  - (a) complements of SEQ ID NO: 1-44;
  - 10 (b) reverse complements of SEQ ID NO: 1-44;
  - (c) reverse sequences of SEQ ID NO: 1-44;
  - (d) sequences that are 100-mers of a sequence of SEQ ID NO: 1-44;
  - (e) sequences that are 40-mers of a sequence of SEQ ID NO: 1-44; and
  - (f) sequences that are 20-mers of a sequence of SEQ ID NO: 1-44.
- 15 3. An isolated polynucleotide comprising a sequence selected from the group consisting  
of:
  - (a) sequences having at least 75% identity to a sequence of SEQ ID NO: 1-44;
  - (b) sequences having at least 90% identity to a sequence of SEQ ID NO: 1-44;
  - 20 (c) sequences having at least 95% identity to a sequence of SEQ ID NO: 1-44;
  - (d) sequences having at least 98% identity to a sequence of SEQ ID NO: 1-44;  
and
  - (e) sequences that hybridize to a sequence of SEQ ID NO: 1-44 under stringent  
hybridization conditions.
- 25 4. An isolated polypeptide encoded by a polynucleotide of any one of claims 1-3.
5. An isolated polypeptide comprising an amino acid sequence selected from the group  
consisting of: SEQ ID NO: 45-88.

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6. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:
- (a) sequences having at least 75% identity to a sequence of SEQ ID NO: 45-88;
  - (b) sequences having at least 90% identity to a sequence of SEQ ID NO: 45-88;
  - 5 and
  - (c) sequences having at least 95% identity to a sequence of SEQ ID NO: 45-88.
7. An isolated polynucleotide that encodes a polypeptide of any one of claims 5 and 6.
- 10 8. An isolated oligonucleotide probe or primer comprising at least 10 contiguous residues complementary to 10 contiguous residues of a nucleotide sequence recited in any one of claims 1-3.
9. A kit comprising a plurality of oligonucleotide probes or primers of claim 8.
- 15 10. A genetic construct comprising a polynucleotide of any one of claims 1-3.
11. A transgenic cell comprising a genetic construct according to claim 10.
- 20 12. A genetic construct comprising, in the 5'-3' direction:
- (a) a gene promoter sequence;
  - (b) a polynucleotide sequence comprising at least one of the following: (1) a polynucleotide coding for at least a functional portion of a polypeptide of any one of claims 5 and 6; and (2) a polynucleotide comprising a non-coding
  - 25 region of a polynucleotide of any one of claims 1-3; and
  - (c) a gene termination sequence.
13. The genetic construct of claim 12, wherein the polynucleotide sequence is in a sense orientation.
- 30

14. The genetic construct of claim 12, wherein the polynucleotide is in an anti-sense orientation.
15. A transgenic plant cell comprising a genetic construct of claim 12.
- 5 16. A plant comprising a transgenic plant cell according to claim 12, or fruit or seeds or progeny thereof.
17. The plant of claim 16, wherein the plant is selected from the group consisting of:  
10 *Festuca arundinacea* and *Lolium perenne* species.
18. A method for modulating at least one of the fructan composition, cellulose, starch and tannin composition of a plant, comprising modulating the activity of a polypeptide of any one of claims 5 and 6 in the plant.
- 15 19. A method for modulating at least one of the fructan composition, cellulose composition, starch composition and tannin composition of a plant, comprising modulating the activity of a polynucleotide of any one of claims 1-3 in the plant.
- 20 20. The method of claim 19, comprising stably incorporating into the genome of the plant a polynucleotide of any one of claims 1-3.
21. The method of claim 19, comprising stably incorporating into the genome of the plant a genetic construct of any one of claims 10 and 12.
- 25 22. A method for producing a plant having at least one of altered fructan composition, altered cellulose composition, altered starch composition and altered tannin composition, comprising:
- (a) transforming a plant cell with a genetic construct of any one of claims 10 and  
30 12 to provide a transgenic cell; and

- (b) cultivating the transgenic cell, under conditions conducive to regeneration and mature plant growth.

23. A method for modifying the activity of a polypeptide involved in a fructan, cellulose, starch or tannin biosynthetic pathway in a plant, comprising modulating the activity of a polynucleotide of any one of claims 1-3 in the plant.

24. The method of claim 23, comprising stably incorporating into the genome of the plant a genetic construct of claim 12.

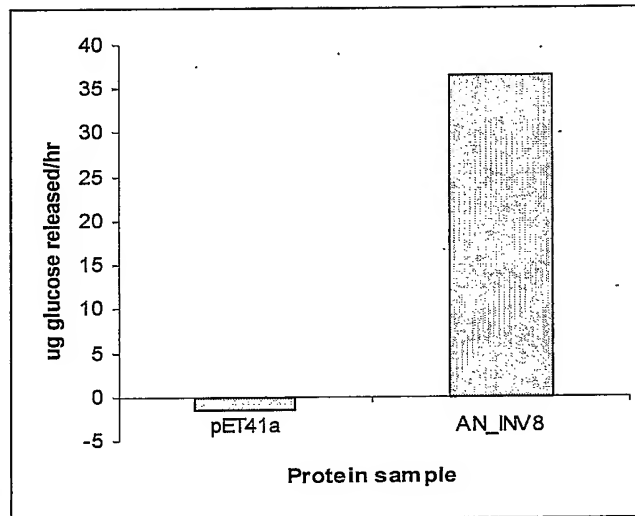
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25. A method for modifying the activity of a polypeptide involved in a fructan, cellulose, starch or tannin biosynthetic pathway in a plant, comprising introducing into cells of the plant double stranded RNA corresponding to a polynucleotide of any one of claims 1-3, thereby inhibiting expression of a polypeptide encoded by the polynucleotide.

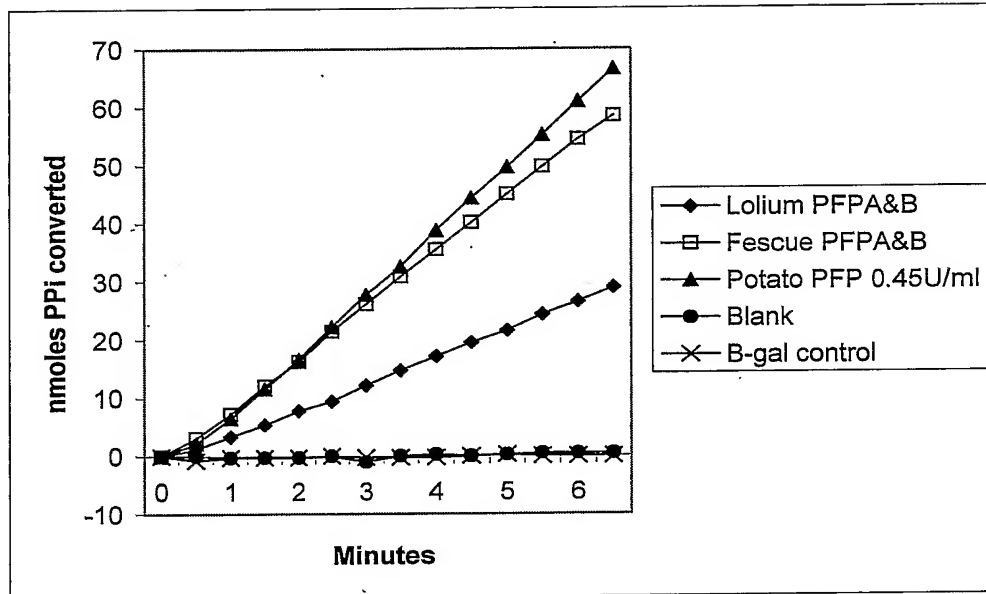
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**Fig. 1**

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**Fig. 2**

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Fig. 3

MAAAAVAPDAKIEKFRDAVAKLGEISENEKAGCISLSVRYLSGEAEQIEWSKIQTPTDEVVVPYDTLAPAP  
 EDLDAMKALLDKLVVLKLNGLGTTMGCTGPKSVIEVRNGFTFLDLIVIQIESLNKKYGCDVPLLLMNSFN  
 THDDTQKIVEKYSNSNINIHTFNQSQYPRIVTEDFLPLPSKQSGKDGWYPPGHGDVFPSSLNNSGKLDTL  
 SQGKEYVVFVANSNDNLGAIVDIKILNHLINNKNEYCMEVTPKTLADVKGGLTISYEGRVQLLEIAQVPDEHV  
 NEFKSIEKFKI FNTNNLWVNLKAIKRLVEADALKMEIIPNPKEVDGVKVLQLETAAGAAIRFFDNAING  
 PRSRFLPVKATSDLLLQSDLYTLVDGYVIRNPARVKPSNPSELGPEFKKVASFLARFKSIPSIVELDSL  
 KVS GDVSFGSGIVLKGNVTIAAKSGVKLEIPDGAVLENKDINGPEDL

Fig. 4

MAAVAADAKIEKFRDAVAKLDEISENEKAGCISLSVRYLSGEAEQIEWSKIQTPTDEVVVPYDTLAPAPQD  
 LDAMKALLDKLVVLKLNGLGTTMGCTGPKSVIEVRNGFTFLDLIVIQIESLNKKYGCDVPLLLMNSFNTH  
 DDTQKIVEKYSNSNINIHTFNQSQYPRIVTEDFLPLPSKQSGKDGWYPPGHGDVFPSSLNNSGKLDTL  
 SQGKEYVVFVANSNDNLGAIVDIKILNHLINNKNEYCMEVTPKTLADVKGGLTISYEGRVQLLEIAQVPDEHV  
 NEFKSIEKFKI FNTNNLWVNLKAIKRLVEADALKMEIIPNPKEVDGVKVLQLETAAGAAIRFFDNAINGPR  
 SRFLPVKATSDLLLQSDLYTLVDGYVIRNPARVKPSNPSELGPEFKKVASFLARFKSIPSIVELDSLKV  
 SGDVTFGSGVVLKGNVTIAAKSGVKLEIPDGAVLENKDINGPEDL

Fig. 5

CLRRRTYSNSGDTHADPNPGPVYGGWYHLFYQHNPYGDWSGNVSWGHAVSKDLVNWRHLPVALVPDQWYDI  
 NGVLTGSI TVLPDGRVILLYTGNTDTFSQVQCLAVPADPSDLLRSWIKHPANPILFPPPGIGLKDFRDP  
 TAWFEHSDNTWRTIIGSKDDDGHAGIVLSYKTTDFVNYELMPGNMHRGPDGTGMYECLDIYPVGGNSSEML  
 GGDSSPEVLFVLKESANDEWHDYALGWFDATANTWTPQDPEADLGIGLRYDWGKYASKSFYDPIKNRRV  
 VWAFVGETDSEQADKAKGWASLMSIPRMVELDKKTRTNLIQWPVEEIEITLRRNVTDLGGITVEAGSVIHL  
 LQGGQOLDIEASFRNLSSDIDALNEADVGFNCSSSAGAAVRGALGPFGLLVFADGRHEQTAAYFYVSKGLD  
 GSSLTHYCHDESRSRAKDVVSRVVGTVPVLDGETFSVRVLVDHSIVQS FVMGGRTTVTSRAYPTEAIYA  
 AAGVYLENNATSATITAEGLVYEMASAEQAFLADD

Fig. 6

MESSAVVPGTTAPLLPYDSRENQSSGGGVVWRACAASAVVLLVVVGFFAGGRVDLGQAGEVSATSSVPAA  
 MMEIPRSRGKNFVSEKADGGFPWSNAMLQWQHTGFHFQPLKHYMNDPNPGPVYGGWYHLFYQHNPYGDWS  
 GNVSWGHAVSKDLVNWRHLPVALVPDQWYDINGVLTGSI TVLPDGRVILLYTGNTDTFSQVQCLAVPADPS  
 DLLRSWIKHPANPILFPPPGIGLKDFRDP TAWFEHSDNTWRTIIGSKDDDGHAGIVLSYKTTDFVNYEL  
 MPGNMHRGPDGTGMYECLDIYPVGGNSSEMLGGDSSPEVLFVLKESANDEWHDYALGWFDATANTWTPQD  
 PEADLGIGLRYDWGKYASKSFYDPIKNRRVVWAFVGETDSEQADKAKGWASLMSIPRMVELDKKTRTNLI  
 QWPVEEIEITLRRNVTDLGGITVEAGSVIHLPLQGGQOLDIEASFRNLSSDIDALNEADVGFNCSSSAGAAV  
 RGALGPFGLLVFADGRHEQTAAYFYVSKGLD GSSLTHYCHDESRSRAKDVVSRVVGTVPVLDGETFSVR  
 VLVDHSIVQS FVMGGRTTVTSRAYPTEAIYAAAGVYLFNNATSATITAEGLVYEMASAEQAFLADD

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Fig. 7

**MATAAAAAALIPHLGCSDA**APRRPGNSLRAHLRKGGIRGRRRSPPCAVNSLHPSGNPKTPGGGDVGGAWGL  
 NGGATAKPDHAPPSQRRRAPRDVEEEAWALLRESVSVSYCGSPVGTIAACDPNDASPLNYDQVFIRDFVPSG  
 VAFLLKGEHEIVRNFIHLTLQLQSWEKTI DCHSPGQGLMPASFVKVRVPLDGGDDGATEEVLDPDFGEAAI  
 GRVAPVDSGLWWIILLRAYGKCSGDL SFHERVDVQTGIKLILKLCLADGDFMFP TLLVTDGSCMMDRRMGI  
 HGHPLEIQALFY SALLSAREMLTPEDGSADLIRALNSRLMALS FHI REYYWLEKRKLNEIYRYKTEEYSYD  
 AVNKFNIYPDQIP PWLVEWI PPKG GYFIGNLQPAHMDFRFFSLGNLWSIVSSLATADQSHAILDLVEAKWS  
 DLVAEMPMKICYPALEDQEWKFITGSDPKNTPWSYHNGGSWPTLLWQLTVACIKMNRPEIAARAVEVAESR  
 ISMDKWPEYYDTKRGRFIGKQARLFQ TWSIAGFLVAKLLENPEKS RILWNNDEEILNALSLMTGPSSPK  
 RKRGRKTYIV

Fig. 8

**MNGQTTMGLAAAAAAVRF**CCRRRLSSASAAAAAKASATPLFPRCSHPQHQQHSRRI PFLVSAASHTSQSD  
 PSTTPTPVTSDPRS AVAGNLPFFDRVLFPGSFPLETPPVEEPAPAPPADAEQASASPVREESDTEREAWRL  
 LRRAVSVSYCGDPVGTVA AEDPECTEMLNYDQVFIRDFVPSALAFLMRGETEIVRNFLH TLQLQSWEKTV D  
 CYS PGQGLMPASF KIKTVPLDENNEAFEEVLDPDFGESAI GRVAPVDSGLWWIILLRAYCKFTGDYSLQER  
 VDVQTGIKLILSLCLTDGDFMFP TLLVTDGSCMIDRRMGIHGHPLEIQALFY SALLSAREMLTPEDGSADLIRALNSRLMALS  
 FHI REYYWVDMKKINEIYRYKTEEYSHDATNKFNIYPEQIPSWLVDWVPEKGGYLI GN L  
 LQAINNRLSALS FHI REYYWVDMKKINEIYRYKTEEYSHDATNKFNIYPEQIPSWLVDWVPEKGGYLI GN L  
 QPAHMDFRFFSLGNLWAISSSLTPTQAEGILSLIEEKWDDL VANMPLKICYPAMEDDEWRIVTGS DPKNT  
 PWSYHNGGSWPTLLWQFTLACIKMGRPELARRAIAVAEEKLSADKWPEYYDTRSGRFVVGKQSRSYQTWTIA  
 GFLT SKILLENPELASILTCEDELELLEGACCLSKRTRCSRRVTKSDIIG

Fig. 9

**MATAAAAAALIPHLGCSDA**APRRPGNSLRAHLRKGGIRGRRRSPPCAVNSLHPSGNPKTPGGGDVGGGRGV  
 NGGATAKPDHAPPSQRRRAPRDVEEEAWALLRESVSVSYCGSPVGTIAACDPNDASPLNYDQVFIRDFVPSG  
 VAFLLKGEHEIVRNFIHLTLQLQSWEKTI DCHSPGQGLMPASFVKVRVPLDGGDDGATEEVLDPDFGEAAI  
 GRVAPVDSGLWWIILLRAYGKCSGDL SFHERVDVQTGIKLILKLCLADGDFMFP TLLVTDGSCMMDRRMGI  
 HGHPLEIQALFY SALLSAREMLTPEDGSADLIRALNSRLMALS FHI REYYWLEKRKLNEIYRYKTEEYSYD  
 AVNKFNIYPDQIP PWLVEWI PPKG GYFIGNLQPAHMDFRFFSLGNLWSIVSSLATADQSHAILDLVEAKWS  
 DLVAEMPMKICYPALEDQEWKFITGSDPKNTPWSYHNGGSWPTLLWQLTVACIKMNRPEIAARAVEVAESR  
 ISTDKWPEYYDTKRGRFIGKQARLFQ TWSIAGFLVAKLLENPEKS RILWNNDEEILNALSLMTGPSSPK  
 RKRGRKTYIV

Fig. 10

MKRVSSHVSIASEAEINLDLSRL LIDKPRYTLEKRSFDEQSWSELTHTRQNDGFD SVLQSPA FRTGFD S  
 PFSMGT HFGEP SGPHPLVNEAWEALRKS VVYFRGQPVGTIAAVDHASEEVLNYDQVFVRDFVPSALAF LMN  
 NEPEIVKNFLLKTLHLQSSEKMVD RFKLGAGAMPA SFKVRNKS RNTETLVADFGESAIGRVAPVDSGFWW  
 IILLRAYTKYTG DASLSESPDCQKCMRLILNLCLSEGFDTFPTLLCTDGCSMIDRRMGIYGYPIEIQALFY  
 MALRCALQMLKPDGEKDFIEKIGORLHALTYHMRNYFWLDFPHLNNIYRYKTEEYSHTAVNKFNVIPDSI  
 PDWVFDFMPCRGGYFLGNVSPAMMDFRWFALGNCAIALISSLATPEQSSAIMDLIEERWDELVGEVPLKICY  
 PAIENHEWRIITGCDPKNTRWSYHNGGSWPTLLWQLTVACIKMNRPEIAARAVEVAESR  
 KLKGFVVGKQARKFQTWSIAGYLVARMMLLED PSTLMMISMEEDRPVKPTMRRSASWNA

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Fig. 11

MEAPGGGAGEMPPTTPSHASIASDDFDLSRLLNHRPRINVERQRSFDDRSISLDLYLSAMDSRGGYMDSYDS  
 MYSPGGGLRSLTGTTPASSTRLSFEPQLLVAAEALRRSLVCFRGEPLGTIAAVDSSSDEVLNVDQVFVRD  
 FVPSALAFMLNGEPDIVKNFLKTLTLLQGWEKRIDRFKLGEAMPASFKVLKDPKRGVDTLAADFGESAIG  
 RVAPADSGFWWIILLRAYTKSTGDLTLAETPECQKGIRLIMNQCLAEGFDTFPTLLCADGCCMIDRRMGVY  
 GYPIEIQALFFMSLRCALLLLKPAVEGNSSSKDDDIMERIVTRLHALSYHMRSYFWLDFQQLNVIYRFKTE  
 EYSHTAVNKFNVIPESIPDWLFDMPSPRGGYFVGNVSPARMDERWFALGNCVAILASLATPEQAGAIMDLI  
 EERWEDLIGEMPLKICYPTIEGHEWQNVTCDPKNTRWSYHNGGSWPVLLIWLITAAACIKTGRCLKIARRAID  
 LAEARLGKDGWPEYYDGKLGKRYVVGKQARKHQTWSIAGYLVAKMMLEDPSHLGMIS

Fig. 12

MEFGAPGGMRRSASHNSLSGSDDFDLTHLLNKPRINVERQRSFDDRSISDVSYSGGGHARGAGGGFDGMYS  
 PGGGLRSLVGTTPASSALHSFEPHPIVGDAWEALRRSLVFFRQPLGTIAAYDHASEEVLNVDQVFVRDFVP  
 SAMAFMLNGEPEIVKNFLKTVLLQGWEKKVDRFKLGEAMPASFKVLHDDKKGVDTLHADFGESAIGRVA  
 PVDSGFWWIILLRAYTKSTGDLTLAEKPECQKAMRLILSLCLSEGFDTFPTLLCADGCCMIDRRMGVYGY  
 IEIQSLFFMALRCALLMLKHDNEGKDFVERIATRLHALSYHMRSYFWLDFQQLNDIYRYKTEEYSHTAVNK  
 FNVIPDSIPDWLFDMPCEGGFFVGNVSPARMDERWFALGNMIAIVSSSIATPEOSTAIMDLIEERWEELIG  
 EMPLKICYPAIENHEWRIVTGCDPKNTRWSYHNGGSWPVLLIWLITAAASIKTGRPQTARRAIDLAERRLLKD  
 GWPEYYDGKLGKRYVVGKQARKFQTWSIAGYLVAKMMLEDPSHLGMIALEEDKAMKPVLRSSASWTN

Fig. 13

MDSYGVPRELSEVQKKRTLYQPDLPCLQGTTVRVEYGDVAIAADPAGAHVISHAFPHTYGOPLAHFLRK  
 AANVADAKVISEHPAVRVGIVFCGRQSPGGHNVIWGLHDAIKAHNPNNSKLIGFLGGSDDLAAOKTLEITDE  
 VLSSYKNQGGYDMLGRTKDQIRTEQVNGAMASCOALKLDALIIIGGVTSNTDAAQLAETFAEAKCATKV  
 GVPVTLNGDLKNQFVETTVGFDTICKVNSQLISNMCTDALSAEKYYYFIRMMGRKASHVALECALQSHPNM  
 VILGEEVAASKLTI FDI TKQICDAVQARAEDKNHGVILPEGLVESIPELYALLQEINGLHGKGVSIENI  
 SSQSPWASALFEFLPQFIRQQLLRPESDDSAQLSQIETEKLLAQIVETEMNKRLEKGTGKGFNAICH  
 FFGYQARGAMPKSFDCDYAYVLGHVSYHILAAGLNGYMATVTNLKSPLNKWRCGAAPISSMNTVKRWSRGP  
 STTQIGKPAVHMASVDLRGKAYELLRONSSSCLLEDIYRNPGLQFEGPGSDSKPISLCVEDQDYMGRICK  
 LQEYLEKVKSIKPGCSQDVLKAALSAMSSVTDTLAIMTSSSTGOAPL

Fig. 14

MDSYGVPRELSEVQKKRTLYQPELPCLQGTTVRVEYGDVAIAADPAGAHVISHAFPHTYGOPLAHFLRK  
 AANVADAKVISEHPAVRVGIVFCGRQSPGGHNVIWGLHDAIKAHNNSNSKLIGFLGGSDDLAAOKTLEITDE  
 VLSSYKNQGGYDMLGRTKDQIRTEQVNGAMASCODLKLDAALIIIGGVTSNTDAAQLAETFAEAKCATKV  
 GVPVTLNGDLKNQFVETTVGFDTICKVNSQLISNMCTDALSAEKYYYFIRMMGRKASHVALECALQSHPNM  
 VILGEEVAASKLTI FDI TKQICDAVQARAEDKNHGVILPEGLVESIPELYALLQEINGLHGKGVSIENI  
 SSQSPWASALFEFLPQFIRHQLLRPESDDSAQLSQIETEKLLAQIVETEMNKRLEKGTGKGFNAICH  
 FFGYQARGAMPKSFDCDYAYVLGHVSYHILAAGLNGYMATVTNLKSPLNKWRCGAAPISSMNTVKRWSRGP  
 STTQIGKPAHMATVDLRGKAYELLRONSSSYLLEDIYRNPGLQFEGPGADSKPISLCVEDQDYMGRICK  
 LQEYLEKVKSIKPGCSQDVLKAALSAMSSVTETLAIMTSSSTGOAPL

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Fig. 15

MAAAAVATSN GASANGPTPGRLASVYSEVQTSRIAHALPLPSVLRSHFTLADGAASSATGNPEEIAKLFNP  
 LYGPQSAAVVPSAQPVATKPLKIGVVLSSGGQAPGGHNVICGIFDYLOERAKGSTMYGFKGGPAGVMKGKYV  
ELNADFVYPYRNQGGFDMICSGRDKIETPEQFQKQAEDTVTKLDLDGLVVI GGDDSN TNACLLGEYFRGRNL  
KTRVIGCPKTIDGDLKCKEVPTSFGFDTACKIYSEMIGNVMTDARSTGKYYHFVRLMGRAASHITLECALQ  
THPNVSLIGEEVAEKKETLQVTDYITDVICKRAELGYNYGVLIPEGLIDFIPEVOKLIAELNEILAHDV  
 VDEAGAWKSKLQEPESRQLFDLFPNTIQEQLLERDPHGNVQVAKIETEKMLIAMVETELEKRRSAGKYSAH  
 FRGQSHFFGYEGRCGLPTNFDSSYCYALGYGAGALLQFGKTGLISSVGNLAAPVEEWTVGGTPLTALMDVE  
 RRHGKFKPVIKKAMVELDAAPFKKFASMRDEWAIKNRYISP GPIQFSGPGSDASNHTLMLELGAQT

Fig. 16

MAAAAVATSN GASANGPTPGRLASVYSEVQTSRIAHALPLPSVLRSHFTLADGAASSATGNPEEIAKLFNP  
 LYGPQSAAVVPSAQPVATKPLKIGVVLSSGGQAPGGHNVICGIFDYLOERAKGSTMYGFKGGPAGVMKGKYV  
ELNADFVYPYRNQGGFDMICSGRDKIETPEQFQKQAEDTVTKLDLDGLVVI GGDDSN TNACLLGEYFRGRNL  
KTRVIGCPKTIDGDLKCKEVPTSFGFDTACKIYSEMIGNVMTDARSTGKYYHFVRLMGRAASHITLECALQ  
THPNVSLIGEEVAEKKETLQVTDYITDVICKRAELGYNYGVLIPEGLIDFIPEVOKLIAELNEILAHDV  
 VDEAGAWKSKLQEPESRQLFDLFPNTIQEQLLERDPHGNVQVAKIETEKMLIAMVETELEKRRSAGKYSAH  
 FRGQSHFFGYEGRCGLPTNFDSSYCYALGYGAGALLQFGKTGLISSVGNLAAPVEEWTVGGTPLTALMDVE  
 RRHGKFKPVIKKAMVELDAAPFKKFASMRDEWAIKNRYISP GPIQFSGPGSDASNHTLMLELGAQT

Fig. 17

MAAAAVATSN GASANGPTPGRLASVYSEVQTSRIAHALPLPSVLRSHFTLADGPASSATGNPEEIAKLFNP  
 LYGPQSAAVVPSAEPVPTKPLKIGVVLSSGGQAPGGHNVICGIFDYLOERAKGSTMYGFKGGPAGIMKGKYI  
ELNADFVYPYRNQGGFDMICSGRDKIETPEQFQKQAETVNKL DLDGLVVI GGDDSN TNACLLGEYFRGRNL  
KTRVIGCPKTIDGDLKCKEVPISTFGFDTACKIYSEMIGNVMTDARSTGKYYHFVRLMGRAASHITLECALQ  
THPNVSLIGEEVAEKKETLQVTDYITDVICKRAELGYNYGVLIPEGLIDFIPEVOKLIAELNEILAHDV  
 VDEAGAWKSKLQEPESRQLFDLFPNTIQEQLLERDPHGNVQVAKIETEKMLIAMVETELEKRRSAGKYSAH  
 FRGQSHFFGYEGRCGLPTNFDSSYCYALGYGAGALLQFGKTGLISSVGNLAAPVEEWTVGGTPLTALMDVE  
 RRHGKFKPVIKKAMVELDAAPFKKFASMRDEWAIKNRYISP GPIQFSGPGSDASNHTLMLELGAQT

Fig. 18

MVGNDNWINSYLDAILDAGKSSIGGDRPSLLLLRERGHFSPARYFVEEVITGYDETDL YKTLWRANAMRSPQ  
 ERNTRLENMTWRIWNLARKKKELEKEEACRLLKRHPETEKTRTDATADMSEDLFDGEKGEDAGDPSVAYGD  
 STTGSSPKTSSVDKLYIVLISLHGLVRGENMELGRDSDTGGQVKYVVEFAKALSSSPGVYRVDLLTROIVA  
 PNFDRSYGEPEEMLVSTTFKNSKHERGVNSGGYIIRIPFGPKDKYLAKHEHWPFIQDFVDGALSHILRMSK  
 TIGEEIGCGHPVWPAVINGHYASAGVAAALLSGALNLPMAFTGHFLGKDKLEGLLKQGRSREQINMTYKI  
 MRRIEAEELSLDASEIVIASTRQEIIEQWNLYDGFEVILARKLRARVVRGANCYGRYMPRMVIPPGEVEFG  
 HVVHDFDMDGEEENHGPASEDPPIWSQIMRFFTNPRKPMILAVARPYPEKNITSLVKAFGECCRPLRELANL  
TLIMGNREAIKMHNTSASVLTSLTLIDEYDLYGQVAYPKHHKHSEVPDIYRLATRTKGAFVNVAYFEQF  
GVTLIEAAMNGLPVIATKNGAPVEINOVLNGLLVDPHDQNAIADALYKLLSEKQLWSRCRENGLNIHQF  
 SWPEHCKNHLRILTLGARSIPAIGSKEERSNAPISGRKHIIIVISVDSVNKEDLVRIIRNAIEAAHTQNTPA  
 STGEVLSTSLTLSEICSLLVSGMHPAGFDAFICNSGSSIIYPSYSGNTPSSSKVTHVIDQNHQSHIEYRW  
 GGEGLRKYLKWKATSVVERKGRIERQMI FEFDEHSSTYCLAFKVVNPNHLPPLKELRKL MRIQSLRCNALY  
 NHSATRLSVTPIHASRSQAIRYLFIRWGIELPNIVVLVGESGSDSYELLGGLHRTIILKGFDFNIAANRIH  
 TVRRYPLQDVVALDSSNIIIEVEGCTTDVIKSALRQIGVPTQ

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Fig. 19

MVGGMCGNDNWINSYLDAILDAGKGAPGGGAGPGGGRGGGGGAGDRPSLLLRERGHFSPARYFVEEVITG  
 YDETDLYKTWSRANAMRSPQERNTRLENMTWRIWNLARKKKEXEAEANRLKRRLETEKPRTDAAAEMSE  
 DLFEQGKGEDAGDASVAYGDSSASNTPRISSIDKLYIVLISLHGLVRGENMELGRSDSTSGQVKYVVELAK  
 ALSSCPGVYRVDLLTRQILAPNYDRGYGEPSETLLPTNLKNFKHERGENSGAYITRIPIFGPKDKYLAKQL  
 WPYVQEFVDGALSHIVRMSKTIGEEIGCGHPMWPAAIHGHYASAGVAAALLSGALNVHMIETGHFLGRDKL  
 EGLLKQKGKOTREEINMTYKIMRRIEAEELSLSLASEIVIASTRQEIIEQWNLYDGFVMLARKLRARVKRGA  
 NCYGRYMPRMVVIIPPGVEFGHMIQDFDMDGEEDSPSPASEDPPIWSEIMRFFTNPRKPLILAVARPYPEKN  
ITTLVRAFGECPRLRELANLTLIMGNREAIKMSNMMSAAVLTSVLTLLIDEYDLYGQVAYPKHHKHSEVLDI  
YRLAARTKGAFVNVAYFEQFGVTLLIEAAMHGLPVIATKNGAPVEIHQVLLNGLLVDPHDONAIADALYKLL  
SEKOLWSRCRENGLKNIHQFSWPEHCKNYLSRIITLSPRYPAFASNDQIKAPIKGRKYIIVIAVDSASKK  
 DLAFIIRNSIEATRTESSSGSTGEVLTSLTITSEIHSLLISAGMVPTDFDAFICNSGSDLFYPSQTGSDPS  
 TSRVTFALDRNYQSRVEYHWGGEGLRKYLKWKASSVVERRGRMEKQVIFDDSEHSSTCCLAFRVVNPNYLP  
 PLKELQKLMRVQSLRCHALYNHSATRLSVIPIHASRSQAIRYLSVRWGIELPNVVLVGESGSDSYEELFG  
 GLHKTVVNLNGEFNTPANRIHTVRRYPLQDVIALDCSNIVGVQGCSTDCMRSTLEKLGIPTK

Fig. 20

MVRGGGNGEVELSVGAGGGGGGAGGLVEPPVPISLGRVLVAGMVAGGVQYGWALQLSILLTPYVQTLGLSHA  
LTSEFMWLCGPIAGLVVQPCVGLYSDKCTSRWGRRRPFIMTGCVLICIAVVIVGFSADIGAALGDSKEECSL  
 YHGPRWHAIAIVYVLGFWLLDFSNNTVQGPALMADLSGKYGPSAANSIFCSWMALGNILGYSSGSTDKWH  
 KWFPFLRTRACCEACANLKGAFLVAVLEFLCMCLVITLIFAKEVPYKRIAPLPTKANGQVEVEPSGPLAVFQ  
 GIRNLPSCMPSVLLVTGLTWLSWFPEFLYDTDWMGREIYHGDPKGTPAEASAFQDGVRAAGFGLLLNSIIL  
GFSSFLIEPMCKRLGPRVVWVSSNLLVCIAMAATAIISWWSTKEFHEYVQHAIITASKDIKIVCMALFAFLG  
VPLAILYSVPFAVTAQLAASKGGGQGLCTGVNLISIVIPOVIALGAGPWDQLFGKGNIPAFAAASAFALI  
GGIVGIFLLPKISRRSFRAVSTGGH

Fig. 21

ICVAVVVVGFESADIGAALGDSKEECSLYHGPRWHAIAIVYVLGFWLLDFSNNTVQGPALMADLSGKYGPS  
AANSIFCSWMALGNILGYSSGSTDKWHKWFPFLRTRACCEACANLKGAFLVAVLEFLCFCLVITLIFAKEVP  
 YKRIAPLPTKANGQVEVEPSGPLAVFQGFRLNLPSCMPSVLLVTGLTWLSWFPEFLYDTDWMGREIYHGDPK  
 GTPAEASAFQDGVRAAGFGLLLNSIILGFSSFLIEPMCKRLGPRVVWVSSNLLVCIAMAATAIISWWSTKE  
 FHEYVQHAIITASKDIKIVCMVLEAFGLVPLAILYSVPFAVTAQLAANKGGGQGLCTGVNLISIVIPOVIAL  
LGAGPWDQLFGKGNIPAFAAASAFALIGGIVGIFLLPKISRRSFRAVSTGGH

Fig. 22

MVRGGGNSEVELSVGAGGGGGGAGGLVEPPVPISLGRVLVAGMVAGGVQYGWALQLSILLTPYVQTLGLSHA  
LTSEFMWLCGPIAGLVVQPCVGLYSDKCTSRWGRRRPFIMTGCVLICIAVVIVGFSADIGAALGDSKEECSL  
 YHGPRWHAIAIVYVLGFWLLDFSNNTVQGPALMADLSGKYGPSAANSIFCSWMALGNILGYSSGSTDKWH  
 KWFPFLRTRACCEACANLKGAFLVAVLEFLCFCLVITLIFAKEVPYKRIAPLPTKANGQVEVEPSGPLAVFQ  
 GFRNLPSCMPSVLLVTGLTWLSWFPEFLYDTDWMGREIYHGDPKGTPAEASAFQDGVRAAGFGLLLNSIIL  
GFSSFLIEPMCKRLGPRVVWVSSNLLVCIAMAATAIISWWSTKEFHEYVQHAIITASKDIKIVCMVLEAFGLG  
VPLAILYSVPFAVTAQLAANKGGGQGLCTGVNLISIVIPOVIALGAGPWDQLFGKGNIPAFAAASAFALI  
GGIVGIFLLPKISRRSFRAVSTGGH

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Fig. 23

MPPRRPTTGGTTTTSAALPPPRKVPLRSLRAASVACGVQFGWALQSLSTPYVQELGIPHAFASLVWLC  
GPLSGLIVQPLIGHLSDRIPADSPLGRRRPFIAAGAASIAFSVLTVGFSADLGRLFGDNVRPGSTRYGAI  
TVYMIGFWLLDVGNNAATQGPCRAFLADLTENDPRRTRIANAYFSLFMALGNILGYATGAYSGWYKIFPFTI  
TESCGVSCANLKSASFLLDIIILAITTYVTVTVDNPTFGSDEAAPRPSSEEEAFLFELFGSFKYFTMPV  
WMVLIVTSLTWIGWFFFLFDTDWMGREIYRGSPEIVADTQKYHDGVRMGSGFLMLNSVLLGITSVVT  
TEKLCRWGAGLVWGVSNIMALCFVAMLIITYVAQNLDYGPSGAPPTGIVVASLTVFTILGAPLSITYSIPYAM  
ATSRVENLGLGQGLAMGILNLSIVIPQIIIVSLGSGPWDSLFGGGNAPSFVWAAAASF  
IGGLVAAILGLPRAR  
 IAPKKRSQR

Fig. 24

MPPRRPNAGGTTSAPLPPPRKVPLRSLRAASVACGVQFGWALQSLSTPYVQELGIPHAFASLVWLCGP  
LSGLIVQPLIGHLSDRIPADSPLGRRRPFIAAGAASIAFSVLTVGFSADLGRLFGDNIRPGSTRFGAIIV  
YMIGFWLLDVGNNAATQGPCRAFLADLTENDPRRTRIANAYFSLFMALGNILGYATGAYSGWYKIFPFTITE  
SCGVSCANLKSASFLLDIIILAITTYVTVTVDNPTFGSDEAAPRPSSEEEAFLFELFGSFKYFTLPVWM  
VLIVTSLTWIGWFFFLFDTDWMGREIYRGSPEIVADTQKYHDGVRMGSGFLMLNSVLLGITSVVM  
MEKLCRWGAGLVWGVSNIMALCFVAMLIITYVAKNLDYGPSGAPPTGIVVASLAVFTILGAPLSITYSIPYAMAT  
SRVENLGLGQGLAMGILNLSIVIPQIIIVSLGSGPWDSLFGGGNAPSFVWAAAASF  
IGGLVAAILGLPRARIA  
 PKKRSQR

Fig. 25

MVDQDHDGRRRQEEATAVAASSVPLLEKKPGDVPYYVEGCPGCAVDRRKATDPGIPYGSFIYIWWVILCTA  
IPISSLFPFLYFMIRDLHIAERTEDIGFYAGFVGAAFMEGRCLTSTIWGIAADRIGRKPVVIFGVFSVVIF  
NALFGLSVTYWMAIATRFLLGALNGLLGPMKAYATEVCRPEHEALALSLVSTAWGIGLIIGPALGGYLALP  
AEKYPNIFSPDSLFCRFPYFLPCLCTSVFAAAVLIGCIWMPETLHKHKVNENRNQSVESLEAHLIDPKEKV  
EQSNSPDTKKSLFKNWFLMSSIIIVYCVFSFHDMAYTEVFSLWAESDRTYGGLSLSSSDVGOITLAITGSSLL  
VYQFLYPRINRVLGPICKSSQIAAGICIPILFAYPYMTYLSEPGLSIVLNIA SVIKNNLGVTIITGTFILQ  
NNAVPQDQORGAANGLAMTGMSFEKAVAPAGAGIVESWAQKROHAFFFPQDOMVFLLNIIELLGLLLTFKE  
FLAVPDKSDSN

Fig. 26

MSSMQFSSVLPLEGKACVCPVRSANNGCERLKVGDSSSLRHEMALRRKCNGARGGGAADGAQCVLTS  
DASPDTLVVRSSFRMNYADPNEVAAVILGGGTGTOLFEPLTSTRATPAVPIGGCYRLIDIPMSNCFNSGINKIFVM  
TQFNSASLNRIHRTYLGGGINFTDGSVEVLAATQMPGEAAGWFRGTADAVRKFTWVLEDYKHKHSIEHIL  
ILSGDQLYRMDYMEIVQKHVDDNADITLSCAPVGE SRASEYGLVKFDS SGRVIOFSEKPKGADLEAMKVD  
T SFLNFAIDDPKPNPYIA SMGVYVFKREVLLNLLKSRYTELHDFGSEILPRALHDHNVQAYVFTDYWEDIGT  
IRSFDDANMALCEQP PKFEFYDPKTPFFTSPRYLPPTKSDKCRIKEAII SHGCFRECTIEHSIIIGVRSRL  
NSGSVLKNAMMMGADLYETEDI SGLLSEGVPIGVGENSKLSNCIIDMNARIGRDVVIANSEGVQEADRP  
 EGGYIRSGIVVILKNATVKDGTVV



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Fig. 27

MSSMQFSSSVLPLEGKACVCPVRSANNGCERLKVGDSSSLRHEMALRRKCNCGARGGGAADGAQCVLTSASP  
 DTLVVRSSFRMNYADPNEVAAVILGGGTGTOLFPLTSTRATPAVPIGGCYRLIDIPMSNCFNSGINKIFVM  
 TQFNSASLNRHIHRTYLGGGINFTDGSVEVLAATQMPGEAAGWFRGTADAVRKFIWVLEDYKHKHSIEHIL  
 ILSGDQLYRMDYMELVQKHVDDNADITLSCAPVGE SRASEYGLVKFDSSGRVIQFSEKPKGADLEAMKVDI  
 SFLNFAIDDPKNPYIASMGVYVFKREVLLNLLKSRYTELHDFGSEILPRALHDHNVQAYVFTDYWEDIGT  
 IRSFFDANMALCEQPPKFEFYDPKTPFFTSPLYLPPTKSDKCRKEAIIISHGCFLRECTIEHSIIGVRSRL  
 NSGSVLKNAMMMGADLYETEDSGLLSEGKVPPIGVGENSKLSNCIIDMNARIGRDVVIANSEGVQEADRP  
 EEGYYIRSGIVVILKNATVKDGTVV

Fig. 28

MTGAPPSTVMAMGAATSPCKILSATQORASTAAASASTSRESVSLRAPRGRRQRPRRGLALSLAPARRPFV  
 FSPRAVSDSKSSQTCLEPDASTSVLGIILGGGAGTRLYPLTKKRAKPAVPLGANYRLIDIPVSNCLNSNIS  
 KIYVLTQFNSASLNRHLSRAYGSNIGGYKNEGFVEVLAQQSPDNPWFQGTADAVRQYLWLFEEHNVMEY  
 LILAGDHLYRMDYEKFIQAHRETDADITVAALPMDEERATAFGLMKIDEEGRIVEFAEKPKGEQLKAMVD  
 TTILGLDDVRAKEMPYIASMGIYVISKHVMLQLLRDQFPAGANDFGSEVIPGATSTGMRVQAYLYDGYWEDI  
 GTIEAFYNANLGITKKPIPDFSFYDRSAPIYTQPRHLPPSKVLDADVTDSVIGEGCVIKNCKIHHSVGLR  
 SCISEGAIIEDTLIMGADYYETEADKKLLADKGGIPIGIGKNSHIRRAIIDKNARIGDNVKIINVDNVQEA  
 ARETDGYFIKSGIVTVIKDALLPSGTVI

Fig. 29

MTRAPPSTVMAMGAATSPCKILSATQORASAAAPSASTSRESVCLLRAPRGRRQRPRRGLALSLAPARRPFV  
 SPRAVSDSKSSQTCLEPDASTSVLGIILGGGAGTRLYPLTKKRAKPAVPLGANYRLIDIPVSNCLNSNIS  
 IYVLTQFNSASLNRHLSRAYGSNIGGYKNEGFVEVLAQQSPDNPWFQGTADAVRQYLWLFEEHNVMEYL  
 ILAGDHLYRMDYEKFIQAHRETDADITVAALPMDEERATAFGLMKIDEEGRIVEFAEKPKGEQLKAMVD  
 TTILGLDDVRAKEMPYIASMGIYVISKHVMLQLLRDQFPAGANDFGSEVIPGATSTGMRVQAYLYDGYWEDI  
 TIEAFYNANLGITKKPIPDFSFYDRSAPIYTQPRHLPPSKVLDADVTDSVIGEGCVIKNCKIHHSVGLRS  
 CISEGAIIEDTLIMGADYYETEADKKLLADKGGIPIGIGKNSHIRRAIIDKNARIGDNVKIINVDNVQEA  
 RETDGYFIKSGIVTVIKDALLPSGTVI

Fig. 30

MAATMTVEEVKRAQRAEGPATVLAIGTATPANCVYQADYPDYFFKITKSDHLADLKEKFKRMCDKSQIRKR  
 YMHLTEEILEENPNMCAYMAPSLDARQDIVVEVPKLGKAAQAIAKEWGQPRSKI THLVFCTTSGVDMPG  
 ADYQLTKMLGLRPSVKRLMMYQOGCFAGGTVLRLAKDLAENNRGARVLVVCSEITAVTFRGPHEHLSLV  
 GQALFGDGAAAVIIGADPDVSVERPLFQLVSQSQTILPDSEGAIDGHLREVGLTFHLLKDVPGGLISKNIER  
 ALEEFKPLGIDDWNSVFWVAHPGGPAILDMVEAKVNLNKKMRATRHVLSEYGNMSSACVLFIMDEMRRK  
 SAEDGHTTTGEGMDWGVLFEGFGPLTVETTVVLHSMPIAADATA

Fig. 31

MATMTVEEVKRAQRAEGPATVLAIGTATPANCVYQADYPDYFFKITKSDHLADLKEKFKRMCDKSQIRKR  
 YMHLTEEILEENPNMCAYMAPSLDARQDIVVEVPKLGKAAQAIAKEWGQPRSKI THLVFCTTSGVDMPG  
 ADYQLTKMLGLRPSVKRLMMYQOGCFAGGTVLRLAKDLAENNRGARVLVVCSEITAVTFRGPHEHLSLV  
 GQALFGDGAAAVIIGADPDVSVEHPLFQLVSASQTILPDSEGAIDGHLREVGLTFHLLKDVPGGLISKNIER  
 ALEEFKPLGIDDWNSVFWVAHPGGPAILDMVEAKVNLNKKMRATRHVLSEYGNMSSACVLFIMDEMRRK  
 SAEDGHTTTGEGMDWGVLFEGFGPLTVETTVVLHSMPIAAGATA

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Fig. 32

RADLEEESGFDDAVAGCDYAFVLAAPVNLKAENPEKDMVEPAVGGTLNAMRSCVRAGTVKRVVLTSSVASV  
 SARPLLQGDGHVLDDEESWSDVDFLRATKATGHWGYPVSKVLEKAACAFAOASGISLVTVCPVVVVGKAPAV  
 QVHTSVDPVLSPLSGDEAKIQILQHIERASGISLVHVDDL CRAEVFLAEEEA VASGRYICCSLSTTAGVL  
 ARFLSVKYPQYKVRTDRFSGSPEKPRVCMSSAKLVAEGFQYKYKTLDEIYDDVVEYGRALGILP

Fig. 33

MAAAGDGSRRKTACVTGGNGYIASALVKMLLEKGYAVKTTVRNPDDMEKNSHLKDLQALGPLEVFRADLQE  
 EGSFDDAVAGCDYAFVLAAPVNLKAENPEKDMVEPAVGGTLNAMRSCVRAGTVKRVVLTSSVASVSARPLL  
 QGDGHVLDDEESWSDVDFLRATKATGHWGYPVSKVLEKAACAFAOASGISLVTVCPVVVVGKAPAVQVHTSV  
 PDVLSPLSGDEAKIQILQHIERASGISLVHVDDL CRAEVFLAEEEA VASGRYICCSLSTTAGVLARFLSV  
 KYPQYKVRTDRFSGSPEKPRVCMSSAKLVAEGFQYKYKTLDEIYDDVVEYGRALGILP

Fig. 34

FISVTVFYVVGLRQRDLVQAGVQGTINVMRSCVKAGTVKRVILTSSDSAVCQRPLEGDGHVLDDEGSWSDVP  
 YLRAEQPEAWGYAVSKVLMEEAAGKFADENGLGLVSVLPFTTLGAAPVSQARTSVPVVLSLLSGDEEQNLN  
 LEAMHLITESVSIINHIDDL CRAQVFLAENEASSGRYICSSHDTTVVQLARLLADKYPQYNVKSQRFDSPE  
 KPRVCLSSQKLI GEGFVYKYDDLGAILLDDLVEYGRRTTGILPF

Fig. 35

MASAAGRRKTACVTGGSGYIASALIKTLLDHGYAVKTTVRNPDDLEKTSHLKDLOAFGPLEIFRGELDVE  
 GSFDDSVSGCDYVFLVAAPMDMGSINPERDLVQAGVQGTINVMRSCVKAGTVKRVILTSSDSAVCQRPLEG  
 DGHVLDDEGSWSDVPYLRAEQPEAWGYAVSKVLMEEAAGKFADENGLGLVSVLPFTTLGAAPVSQARTSVPV  
 VLSLLSGDEEQNLNLEAMHLITESVSIINHIDDL CRAQVFLAENEASSGRYICSSHDTTVVQLARLLADKYP  
 QYNVKSQRFDSPEKPRVCLSSQKLI GEGFVYKYDDLGAILLDDLVEYGRRTTGILPFAAASIWFLFRGSSSG  
 KKLSKLPLPPGPRGWVFLGNLPQVGAKPHHTMAALSQQFGPLFRFRFGVAE VVAASAKVASQFLRAHDAN  
 FSDRPPNSGAEHVAYNYQDLVFAPYGSRRWRALRKLALHLFSAKALDALRAVREAEVALMVQLKESAPAG  
 VVVGQEANVCATNALARAAGRRVFGGSAGEGAREFKDMVVELMQLAGVFNIGDFVPALRWLDPQGVVARM  
 KRLHRRYDAMMDGFI SERDQRHNQAAADGERKDLSVMLGYMRPDGGGEGEEGIFSNHTDIKALLNLFTA  
 GTDTSSTVEWALAE LIRHKDVLTAQARELDDIVGQDRLVTESDLPHLTFLTAVIKETFRHPSTPLSLPR  
 VATEDCEVEGYRIPKGTTLVNVWAIARDPASWGPDALEFRPARFLAGGLHESVDVKGS DYELIPFGAGRR  
 ICAGLSWGLRMVTLMATLVHAFDWSLVDGLTPEKLDMEEAYGLTLQRAAPLMVRPIPRLLSSAYTV

Fig. 36

MDHRDVLVLLCSLAALAAASIWFLFRGSSSGKKLSKLPLPPGPRGWVFLGNLPQVGAKPHHTMAALSQQFG  
 PLFRFRFGVAE VVAASAKVASQFLRAHDANFSDRPPNSGAEHVAYNYQDLVFAPYGSRRWRALRKLALHL  
 FSAKALDALRAVREAEVALMVQLKESAPAGVVVGQEANVCATNALARAAGRRVFGGSAGEGAREFKDMV  
 VELMQLAGVFNIGDFVPALRWLDPQGVVARMKRLHRRYDAMMDGFI SERDQRHNQAAADGERKDLSVMLG  
 YMRPDGGGEGEEGIFSNHTDIKALLNLFTAGTDTTSSTVEWALAE LIRHKDVLTAQARELDDIVGQDRLV  
 TESDLPHLTFLTAVIKETFRHPSTPLSLPRVATEDCEVEGYRIPKGTTLVNVWAIARDPASWGPDALEFR  
 RPARFLAGGLHESVDVKGS DYELIPFGAGRRICAGLSWGLRMVTLMATLVHAFDWSLVDGLTPEKLDMEE  
 AYGLTLQRAAPLMVRPIPRLLSSAYTV

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Fig. 37

RSELAGMDIPLSLIISTLAISATICYVFFRAGKGHRAPLEPLPPGPRGWPVLGNLPQLGGKTHQTLHEMTKV  
 YGPVLRRLRFGSSVVVVAGSAAVAEQFLRTHDAKFSSRPPNSGGEHMAYNYRDVVFAPYGPWRAMRKVCAV  
 NIFSARALDDLGRFREREALMVRSLADAAKAGVAVAVGKAANVCTTNGLSRAAVGLRVFGSDGARDFKEI  
 VLEVMEVGGVNLNVGDFVPALRWLDPQGVVARLKKLHRRFDDMMNGIIAERRTGKTAVVEEGKGDLLGLLL  
 AMVQEDKSLTGSEEDKITDQDVKALILNLFVAGTETTSSIVWAVAEILRHPDILKQAEELDAVVGRDRL  
 VSESDLPRLTFFNAIIKETFRLLHPSTPLSLPRMASEECEVAGYHIPRGTELLNVNWGIARDPALWDPDLEY  
 QPARFLPGGSHENVDLKGGDFGLIPFGAGRRICAGLSWGLRMVTITTTATLVHSDWELPAGQTPDKLNMEE  
 AFSLLLQRAVPLMVHPVPRLLPSAYEIS

Fig. 38

MRSELAGMDIPLPLLLSTLAISATICYVFFRAGKGHRAPLEPLPPGPRGWPVLGNLPQLGGKTHQTLHEMTK  
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Fig. 39

DIPLPLLLSTLAISATICYVFFRAGKTHQTLHEMTKVYGPVLRRLRFGSSVVVVAGSAAVAEQFLRTHDAKF  
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Fig. 40

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Fig. 41

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## &lt;213&gt; Festuca arundinacea

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&lt;210&gt; 8

&lt;211&gt; 973

&lt;212&gt; DNA

&lt;213&gt; Lolium perenne

&lt;400&gt; 8

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&lt;210&gt; 9

&lt;211&gt; 2019



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<213> *Lolium perenne*

<400> 9

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<213> *Lolium perenne*

<400> 10

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&lt;211&gt; 2143

&lt;212&gt; DNA

<213> *Lolium perenne*

&lt;400&gt; 11

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&lt;211&gt; 2033

&lt;212&gt; DNA

<213> *Lolium perenne*

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&lt;211&gt; 1866

&lt;212&gt; DNA

<213> *Lolium perenne*

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 <213> *Lolium perenne*

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&lt;211&gt; 2179

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&lt;213&gt; Festuca arundinacea

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<212> DNA  
<213> Festuca arundinacea

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&lt;210&gt; 28

&lt;211&gt; 2039

&lt;212&gt; DNA

&lt;213&gt; Lolium perenne

&lt;400&gt; 28

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&lt;211&gt; 2063

&lt;212&gt; DNA

&lt;213&gt; Festuca arundinacea

&lt;400&gt; 29

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 <212> DNA  
 <213> *Lolium perenne*

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<210> 31



<211> 1873  
 <212> DNA  
 <213> Festuca arundinacea

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<210> 32  
 <211> 1494  
 <212> DNA  
 <213> Festuca arundinacea

<400> 32  
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1494

<210> 33  
 <211> 1661  
 <212> DNA  
 <213> Festuca arundinacea

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<210> 34  
 <211> 992  
 <212> DNA  
 <213> Festuca arundinacea

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<210> 35  
 <211> 1279  
 <212> DNA  
 <213> Festuca arundinacea

<400> 35  
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&lt;210&gt; 36

&lt;211&gt; 1206

&lt;212&gt; DNA

<213> *Lolium perenne*

&lt;400&gt; 36

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&lt;210&gt; 37

&lt;211&gt; 1463

&lt;212&gt; DNA

<213> *Lolium perenne*

&lt;400&gt; 37

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 <212> DNA  
 <213> *Lolium perenne*

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<210> 39  
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 <212> DNA  
 <213> *Lolium perenne*

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<210> 40  
 <211> 1747  
 <212> DNA  
 <213> Festuca arundinacea

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<210> 41  
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 <212> DNA  
 <213> Festuca arundinacea

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&lt;210&gt; 42

&lt;211&gt; 1673

&lt;212&gt; DNA

&lt;213&gt; Festuca arundinacea

&lt;400&gt; 42

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&lt;210&gt; 43

&lt;211&gt; 1714

&lt;212&gt; DNA

&lt;213&gt; Festuca arundinacea

&lt;400&gt; 43

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1 Asp	Ala	Val	Ala	Lys	Leu	Gly	Glu	Ile <sup>20</sup>	Ser	Glu	Asn	Glu	Lys <sup>25</sup>	Ala	Gly			
Cys	Ile	Ser	Leu <sup>30</sup>	Val	Ser	Arg	Tyr	Leu	Ser	Gly	Glu	Ala	Glu	Gln	Ile			

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 50 55 60  
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 65 70 75 80  
 Leu Asp Lys Leu Val Val Leu Lys Leu Asn Gly Gly Leu Gly Thr Thr  
 85 90 95  
 Met Gly Cys Thr Gly Pro Lys Ser Val Ile Glu Val Arg Asn Gly Phe  
 100 105 110  
 Thr Phe Leu Asp Leu Ile Val Ile Gln Ile Glu Ser Leu Asn Lys Lys  
 115 120 125  
 Tyr Gly Cys Asp Val Pro Leu Leu Met Asn Ser Phe Asn Thr His  
 130 135 140  
 Asp Asp Thr Gln Lys Ile Val Glu Lys Tyr Ser Asn Ser Asn Ile Asn  
 145 150 155 160  
 Ile His Thr Phe Asn Gln Ser Gln Tyr Pro Arg Ile Val Thr Glu Asp  
 165 170 175  
 Phe Leu Pro Leu Pro Ser Lys Gly Gln Ser Gly Lys Asp Gly Trp Tyr  
 180 185 190  
 Pro Pro Gly His Gly Asp Val Phe Pro Ser Leu Asn Asn Ser Gly Lys  
 195 200 205  
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 210 215 220  
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 Ala Asp Val Lys Gly Gly Thr Leu Ile Ser Tyr Glu Gly Arg Val Gln  
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 Ser Ile Glu Lys Phe Lys Ile Phe Asn Thr Asn Asn Leu Trp Val Asn  
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 Leu Lys Ala Ile Lys Arg Leu Val Glu Ala Asp Ala Leu Lys Met Glu  
 305 310 315 320  
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 Glu Thr Ala Ala Gly Ala Ala Ile Arg Phe Phe Asp Asn Ala Ile Gly  
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 355 360 365  
 Leu Leu Leu Val Gln Ser Asp Leu Tyr Thr Leu Val Asp Gly Tyr Val  
 370 375 380  
 Ile Arg Asn Pro Ala Arg Val Lys Pro Ser Asn Pro Ser Ile Glu Leu  
 385 390 395 400  
 Gly Pro Glu Phe Lys Lys Val Ala Ser Phe Leu Ala Arg Phe Lys Ser  
 405 410 415  
 Ile Pro Ser Ile Val Glu Leu Asp Ser Leu Lys Val Ser Gly Asp Val  
 420 425 430  
 Ser Phe Gly Ser Gly Ile Val Leu Lys Gly Asn Val Thr Ile Ala Ala  
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 35 40 45

Ser Lys Ile Gln Thr Pro Thr Asp Glu Val Val Val Pro Tyr Asp Thr  
 50 55 60  
 Leu Ala Pro Ala Pro Gln Asp Leu Asp Ala Met Lys Ala Leu Leu Asp  
 65 70 75 80  
 Lys Leu Val Val Leu Lys Leu Asn Gly Gly Leu Gly Thr Thr Met Gly  
 85 90 95  
 Cys Thr Gly Pro Lys Ser Val Ile Glu Val Arg Asn Gly Phe Thr Phe  
 100 105 110  
 Leu Asp Leu Ile Val Ile Gln Ile Glu Ser Leu Asn Lys Lys Tyr Gly  
 115 120 125  
 Cys Asp Val Pro Leu Leu Leu Met Asn Ser Phe Asn Thr His Asp Asp  
 130 135 140  
 Thr Gln Lys Ile Val Glu Lys Tyr Ser Asn Ser Asn Ile Asn Ile His  
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 180 185 190  
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 195 200 205  
 Thr Leu Leu Ser Gln Gly Lys Glu Tyr Val Phe Val Ala Asn Ser Asp  
 210 215 220  
 Asn Leu Gly Ala Ile Val Asp Ile Lys Ile Leu Asn His Leu Ile Asn  
 225 230 235 240  
 Asn Gln Asn Glu Tyr Cys Met Glu Val Thr Pro Lys Thr Leu Ala Asp  
 245 250 255  
 Val Lys Gly Gly Leu Ile Ser Tyr Glu Gly Arg Val Gln Leu Leu  
 260 265 270  
 Glu Ile Ala Gln Val Pro Asp Glu His Val Asn Glu Phe Lys Ser Ile  
 275 280 285  
 Glu Lys Phe Lys Ile Phe Asn Thr Asn Asn Leu Trp Val Asn Leu Lys  
 290 295 300  
 Ala Ile Lys Arg Leu Val Glu Ala Asp Ala Leu Lys Met Glu Ile Ile  
 305 310 315 320  
 Pro Asn Pro Lys Glu Val Asp Gly Val Lys Val Leu Gln Leu Glu Thr  
 325 330 335  
 Ala Ala Gly Ala Ile Arg Phe Phe Glu Lys Ala Ile Gly Ile Asn  
 340 345 350  
 Gly Pro Arg Ser Arg Phe Leu Pro Val Lys Ala Thr Ser Asp Leu Leu  
 355 360 365  
 Leu Val Gln Ser Asp Leu Tyr Thr Leu Val Asp Gly Tyr Val Ile Arg  
 370 375 380  
 Asn Pro Ala Arg Val Lys Pro Ser Asn Pro Ser Ile Glu Leu Gly Pro  
 385 390 395 400  
 Glu Phe Lys Lys Val Ala Ser Phe Leu Ala Arg Phe Lys Ser Ile Pro  
 405 410 415  
 Ser Ile Val Glu Leu Asp Ser Leu Lys Val Ser Gly Asp Val Thr Phe  
 420 425 430  
 Gly Ser Gly Val Val Leu Lys Gly Asn Val Thr Ile Ala Ala Lys Ser  
 435 440 445  
 Gly Val Lys Leu Glu Ile Pro Asp Gly Ala Val Leu Glu Asn Lys Asp  
 450 455 460  
 Ile Asn Gly Pro Glu Asp Leu  
 465 470

&lt;210&gt; 47

&lt;211&gt; 535

&lt;212&gt; PRT

<213> *Lolium perenne*

&lt;400&gt; 47

Cys Leu Arg Arg Arg Thr Tyr Ser Asn Ser Gly Asp Thr His Ala Asp  
 1 5 10 15  
 Pro Asn Gly Pro Val Tyr Tyr Gly Gly Trp Tyr His Leu Phe Tyr Gln  
 20 25 30  
 His Asn Pro Tyr Gly Asp Ser Trp Gly Asn Val Ser Trp Gly His Ala  
 35 40 45  
 Val Ser Lys Asp Leu Val Asn Trp Arg His Leu Pro Val Ala Leu Val

50	Pro	Asp	Gln	Trp	Tyr	Asp	Ile	Asn	Gly	Val	Leu	Thr	Gly	Ser	Ile	Thr
65	Val	Leu	Pro	Asp	Gly	Arg	Val	Ile	Leu	Leu	Tyr	Thr	Gly	Asn	Thr	Asp
					85					90					95	
	Thr	Phe	Ser	Gln	Val	Gln	Cys	Leu	Ala	Val	Pro	Ala	Asp	Pro	Ser	Asp
				100					105					110		
	Pro	Leu	Leu	Arg	Ser	Trp	Ile	Lys	His	Pro	Ala	Asn	Pro	Ile	Leu	Phe
			115					120					125			
	Pro	Pro	Pro	Gly	Ile	Gly	Leu	Lys	Asp	Phe	Arg	Asp	Pro	Leu	Thr	Ala
		130					135					140				
	Trp	Phe	Glu	His	Ser	Asp	Asn	Thr	Trp	Arg	Thr	Ile	Ile	Gly	Ser	Lys
145						150					155					160
	Asp	Asp	Asp	Gly	His	Ala	Gly	Ile	Val	Leu	Ser	Tyr	Lys	Thr	Thr	Asp
					165											
	Phe	Val	Asn	Tyr	Glu	Leu	Met	Pro	Gly	Asn	Met	His	Arg	Gly	Pro	Asp
				180					185					190		
	Gly	Thr	Gly	Met	Tyr	Glu	Cys	Leu	Asp	Ile	Tyr	Pro	Val	Gly	Gly	Asn
				195					200				205			
	Ser	Ser	Glu	Met	Leu	Gly	Gly	Asp	Ser	Ser	Pro	Glu	Val	Leu	Phe	Val
		210					215					220				
	Leu	Lys	Glu	Ser	Ala	Asn	Asp	Glu	Trp	His	Asp	Tyr	Tyr	Ala	Leu	Gly
225						230					235					240
	Trp	Phe	Asp	Ala	Thr	Ala	Asn	Thr	Trp	Thr	Pro	Gln	Asp	Pro	Glu	Ala
				245						250					255	
	Asp	Leu	Gly	Ile	Gly	Leu	Arg	Tyr	Asp	Trp	Gly	Lys	Tyr	Tyr	Ala	Ser
				260					265					270		
	Lys	Ser	Phe	Tyr	Asp	Pro	Ile	Lys	Asn	Arg	Arg	Val	Val	Trp	Ala	Phe
			275					280					285			
	Val	Gly	Glu	Thr	Asp	Ser	Glu	Gln	Ala	Asp	Lys	Ala	Lys	Gly	Trp	Ala
		290					295					300				
	Ser	Leu	Met	Ser	Ile	Pro	Arg	Met	Val	Glu	Leu	Asp	Lys	Lys	Thr	Arg
305						310					315					320
	Thr	Asn	Leu	Ile	Gln	Trp	Pro	Val	Glu	Glu	Ile	Glu	Thr	Leu	Arg	Arg
				325						330					335	
	Asn	Val	Thr	Asp	Leu	Gly	Gly	Ile	Thr	Val	Glu	Ala	Gly	Ser	Val	Ile
				340					345					350		
	His	Leu	Pro	Leu	Gln	Gln	Gly	Gly	Gln	Leu	Asp	Ile	Glu	Ala	Ser	Phe
			355					360					365			
	Arg	Leu	Asn	Ser	Ser	Asp	Ile	Asp	Ala	Leu	Asn	Glu	Ala	Asp	Val	Gly
		370					375					380				
	Phe	Asn	Cys	Ser	Ser	Ser	Ala	Gly	Ala	Ala	Val	Arg	Gly	Ala	Leu	Gly
385						390					395					400
	Pro	Phe	Gly	Leu	Leu	Val	Phe	Ala	Asp	Gly	Arg	His	Glu	Gln	Thr	Ala
				405						410					415	
	Ala	Tyr	Phe	Tyr	Val	Ser	Lys	Gly	Leu	Asp	Gly	Ser	Leu	Leu	Thr	His
				420					425				430			
	Tyr	Cys	His	Asp	Glu	Ser	Arg	Ser	Thr	Arg	Ala	Lys	Asp	Val	Val	Ser
		435						440					445			
	Arg	Val	Val	Gly	Gly	Thr	Val	Pro	Val	Leu	Asp	Gly	Glu	Thr	Phe	Ser
		450					455					460				
	Val	Arg	Val	Leu	Val	Asp	His	Ser	Ile	Val	Gln	Ser	Phe	Val	Met	Gly
465					470					475						480
	Gly	Arg	Thr	Thr	Val	Ser	Arg	Ala	Tyr	Pro	Thr	Glu	Ala	Ile	Tyr	
				485					490					495		
	Ala	Ala	Ala	Gly	Val	Tyr	Leu	Phe	Asn	Asn	Ala	Thr	Ser	Ala	Thr	Ile
				500					505					510		
	Thr	Ala	Glu	Gly	Leu	Val	Val	Tyr	Glu	Met	Ala	Ser	Ala	Glu	Ser	Gln
			515					520					525			
	Ala	Phe	Leu	Ala	Asp	Asp	Met									
		530					535									

<210> 48  
 <211> 637  
 <212> PRT  
 <213> Lolium perenne

<400> 48



Met	Glu	Ser	Ser	Ala	Val	Val	Val	Pro	Gly	Thr	Thr	Ala	Pro	Leu	Leu
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Pro	Tyr	Asp	Ser	Arg	Glu	Asn	Gln	Ser	Ser	Gly	Gly	Gly	Val	Trp	Trp
			20					25					30		
Arg	Ala	Cys	Ala	Ala	Ser	Ala	Val	Val	Leu	Leu	Val	Val	Val	Gly	Phe
		35					40					45			
Phe	Ala	Gly	Gly	Arg	Val	Asp	Leu	Gly	Gln	Ala	Gly	Glu	Val	Ser	Ala
	50					55					60				
Thr	Ser	Ser	Val	Pro	Ala	Ala	Met	Met	Glu	Ile	Pro	Arg	Ser	Arg	Gly
65					70					75					80
Lys	Asn	Phe	Gly	Val	Ser	Glu	Lys	Ala	Asp	Gly	Gly	Phe	Pro	Trp	Ser
			85						90					95	
Asn	Ala	Met	Leu	Gln	Trp	Gln	His	Thr	Gly	Phe	His	Phe	Gln	Pro	Leu
			100					105					110		
Lys	His	Tyr	Met	Asn	Asp	Pro	Asn	Gly	Pro	Val	Tyr	Tyr	Gly	Gly	Trp
		115					120					125			
Tyr	His	Leu	Phe	Tyr	Gln	His	Asn	Pro	Tyr	Gly	Asp	Ser	Trp	Gly	Asn
	130					135					140				
Val	Ser	Trp	Gly	His	Ala	Val	Ser	Lys	Asp	Leu	Val	Asn	Trp	Arg	His
145					150					155					160
Leu	Pro	Val	Ala	Leu	Val	Pro	Asp	Gln	Trp	Tyr	Asp	Ile	Asn	Gly	Val
				165					170					175	
Leu	Thr	Gly	Ser	Ile	Thr	Val	Leu	Pro	Asp	Gly	Arg	Val	Ile	Leu	Leu
			180					185					190		
Tyr	Thr	Gly	Asn	Thr	Asp	Thr	Phe	Ser	Gln	Val	Gln	Cys	Leu	Ala	Val
		195					200					205			
Pro	Ala	Asp	Pro	Ser	Asp	Pro	Leu	Leu	Arg	Ser	Trp	Ile	Lys	His	Pro
	210					215					220				
Ala	Asn	Pro	Ile	Leu	Phe	Pro	Pro	Pro	Gly	Ile	Gly	Leu	Lys	Asp	Phe
225					230					235					240
Arg	Asp	Pro	Leu	Thr	Ala	Trp	Phe	Glu	His	Ser	Asp	Asn	Thr	Trp	Arg
				245					250					255	
Thr	Ile	Ile	Gly	Ser	Lys	Asp	Asp	Asp	Gly	His	Ala	Gly	Ile	Val	Leu
			260					265					270		
Ser	Tyr	Lys	Thr	Thr	Asp	Phe	Val	Asn	Tyr	Glu	Leu	Met	Pro	Gly	Asn
		275					280					285			
Met	His	Arg	Gly	Pro	Asp	Gly	Thr	Gly	Met	Tyr	Glu	Cys	Leu	Asp	Ile
	290					295					300				
Tyr	Pro	Val	Gly	Gly	Asn	Ser	Ser	Glu	Met	Leu	Gly	Gly	Asp	Ser	Ser
305					310					315				320	
Pro	Glu	Val	Leu	Phe	Val	Leu	Lys	Glu	Ser	Ala	Asn	Asp	Glu	Trp	His
				325					330					335	
Asp	Tyr	Tyr	Ala	Leu	Gly	Trp	Phe	Asp	Ala	Thr	Ala	Asn	Thr	Trp	Thr
			340					345					350		
Pro	Gln	Asp	Pro	Glu	Ala	Asp	Leu	Gly	Ile	Gly	Leu	Arg	Tyr	Asp	Trp
		355					360					365			
Gly	Lys	Tyr	Tyr	Ala	Ser	Lys	Ser	Phe	Tyr	Asp	Pro	Ile	Lys	Asn	Arg
					375						380				
Arg	Val	Val	Trp	Ala	Phe	Val	Gly	Glu	Thr	Asp	Ser	Glu	Gln	Ala	Asp
385					390					395				400	
Lys	Ala	Lys	Gly	Trp	Ala	Ser	Leu	Met	Ser	Ile	Pro	Arg	Met	Val	Glu
				405					410					415	
Leu	Asp	Lys	Lys	Thr	Arg	Thr	Asn	Leu	Ile	Gln	Trp	Pro	Val	Glu	Glu
			420					425					430		
Ile	Glu	Thr	Leu	Arg	Arg	Asn	Val	Thr	Asp	Leu	Gly	Gly	Ile	Thr	Val
		435					440					445			
Glu	Ala	Gly	Ser	Val	Ile	His	Leu	Pro	Leu	Gln	Gln	Gly	Gly	Gln	Leu
	450					455					460				
Asp	Ile	Glu	Ala	Ser	Phe	Arg	Leu	Asn	Ser	Ser	Asp	Ile	Asp	Ala	Leu
465					470					475				480	
Asn	Glu	Ala	Asp	Val	Gly	Phe	Asn	Cys	Ser	Ser	Ser	Ala	Gly	Ala	Ala
				485					490					495	
Val	Arg	Gly	Ala	Leu	Gly	Pro	Phe	Gly	Leu	Leu	Val	Phe	Ala	Asp	Gly
			500					505					510		
Arg	His	Glu	Gln	Thr	Ala	Ala	Tyr	Phe	Tyr	Val	Ser	Lys	Gly	Leu	Asp
		515					520					525			
Gly	Ser	Leu	Leu	Thr	His	Tyr	Cys	His	Asp	Glu	Ser	Arg	Ser	Thr	Arg
	530					535					540				

Ala Lys Asp Val Val Ser Arg Val Val Gly Gly Thr Val Pro Val Leu  
 545 550 555 560  
 Asp Gly Glu Thr Phe Ser Val Arg Val Leu Val Asp His Ser Ile Val  
 565 570 575  
 Gln Ser Phe Val Met Gly Gly Arg Thr Val Thr Ser Arg Ala Tyr  
 580 585 590  
 Pro Thr Glu Ala Ile Tyr Ala Ala Gly Val Tyr Leu Phe Asn Asn  
 595 600 605  
 Ala Thr Ser Ala Thr Ile Thr Ala Glu Gly Leu Val Val Tyr Glu Met  
 610 615 620  
 Ala Ser Ala Glu Ser Gln Ala Phe Leu Ala Asp Asp Met  
 625 630 635

<210> 49  
 <211> 603  
 <212> PRT  
 <213> Lolium perenne

<400> 49  
 Met Gly Ile Ala Glu Val Ala Leu His Thr Met Pro Gly Ala Phe Ala  
 1 5 10 15  
 Ser His Ser Pro Ala Ser Ser Leu Pro Leu Arg Thr Asp Thr Arg Ser  
 20 25 30  
 Leu Arg Lys Arg Gly Thr Asn Ser Phe Tyr Arg Thr Leu Gly Gly Pro  
 35 40 45  
 Pro Lys Phe Pro Glu Leu Arg Pro Val Glu Cys Gln Cys Gln Arg Ile  
 50 55 60  
 Asp Asp Leu Ala Gly Val Ile Glu Ala Gly Asn Gly Thr Trp Ala Thr  
 65 70 75 80  
 Asp Met Val Asn Lys Ala Ser Gln Val Leu Gly Asp Val Ala Val Pro  
 85 90 95  
 Gly Gln Ala Leu Gly Gly Asn Ala Ser Leu Ser Gly Asp Pro Glu Lys  
 100 105 110  
 Val Leu Pro Arg Arg Arg Asn Leu Ser Ser Val Glu Asp Glu Ala Trp  
 115 120 125  
 Asp Leu Leu Arg Glu Ser Val Val Asn Tyr Cys Gly Ser Pro Val Gly  
 130 135 140  
 Thr Ile Ala Ala Asn Asp Pro Asn Asp Ser Asn Pro Ala Asn Tyr Asp  
 145 150 155 160  
 Gln Val Phe Ile Arg Asp Phe Ile Pro Ser Gly Ile Ala Phe Leu Leu  
 165 170 175 180  
 Lys Gly Glu Tyr Glu Ile Val Arg Asn Phe Ile Leu His Thr Leu Gln  
 185 190 195  
 Leu Gln Ser Trp Glu Lys Thr Met Asp Cys His Ser Pro Gln Gly  
 200 205 210  
 Leu Met Pro Ala Ser Phe Lys Val Arg Thr Ile Pro Leu Asp Gly Asp  
 215 220 225  
 Glu Asn Ala Thr Glu Glu Val Leu Asp Pro Asp Phe Gly Glu Ala Ala  
 230 235 240  
 Ile Gly Arg Val Ala Pro Val Asp Ser Gly Leu Trp Trp Ile Ile Leu  
 245 250 255 260  
 Leu Arg Ala Tyr Gly Lys Cys Ser Gly Asp Leu Ser Val Gln Glu Arg  
 265 270 275  
 Ile Asp Val Gln Thr Gly Ile Lys Met Ile Leu Lys Leu Cys Leu Ala  
 280 285 290  
 Asp Gly Phe Asp Met Phe Pro Thr Leu Leu Val Thr Asp Gly Ser Cys  
 295 300 305  
 Met Ile Asp Arg Arg Met Gly Ile His Gly His Pro Leu Glu Ile Gln  
 310 315 320  
 Ala Leu Phe Tyr Ser Ala Leu Leu Ser Ala Arg Glu Met Leu Thr Pro  
 325 330 335  
 Glu Asp Gly Ser Ala Asp Leu Ile Arg Ala Leu Asn Asn Arg Leu Val  
 340 345 350  
 Ala Leu Ser Phe His Ile Arg Glu Tyr Tyr Trp Val Asp Met Gln Lys  
 355 360 365  
 Leu Asn Glu Ile Tyr Arg Tyr Lys Thr Glu Glu Tyr Ser Tyr Asp Ala  
 370 375 380  
 Val Asn Lys Phe Asn Ile Tyr Pro Asp Gln Val Ser Pro Trp Leu Val

385					390					395					400
Glu	Trp	Ile	Pro	Pro	Lys	Gly	Gly	Tyr	Phe	Ile	Gly	Asn	Leu	Gln	Pro
				405					410					415	
Ala	His	Met	Asp	Phe	Arg	Phe	Phe	Ser	Leu	Gly	Asn	Leu	Trp	Ser	Ile
			420					425					430		
Val	Ser	Ser	Leu	Ala	Thr	Thr	Gln	Gln	Ser	His	Ala	Ile	Leu	Asp	Leu
		435					440					445			
Ile	Glu	Ser	Lys	Trp	Ser	Asp	Leu	Val	Ala	Glu	Met	Pro	Leu	Lys	Ile
	450					455					460				
Cys	Tyr	Pro	Ala	Leu	Glu	Asn	Leu	Glu	Trp	Lys	Ile	Ile	Thr	Gly	Ser
465					470					475					480
Asp	Pro	Lys	Asn	Thr	Pro	Trp	Ser	Tyr	His	Asn	Gly	Gly	Ser	Trp	Pro
				485					490					495	
Thr	Leu	Leu	Trp	Gln	Leu	Thr	Val	Ala	Ser	Leu	Lys	Met	Asn	Arg	Pro
			500					505					510		
Glu	Ile	Ala	Ala	Lys	Ala	Val	Glu	Ile	Ala	Glu	Arg	Arg	Ile	Ala	Thr
		515					520					525			
Asp	Lys	Trp	Pro	Glu	Tyr	Tyr	Asp	Thr	Lys	Arg	Ala	Arg	Phe	Ile	Gly
	530					535					540				
Lys	Gln	Ser	Arg	Leu	Tyr	Gln	Thr	Trp	Ser	Ile	Ala	Gly	Tyr	Leu	Val
545					550					555					560
Ala	Lys	Gln	Leu	Leu	Asp	Lys	Pro	Asp	Ala	Ala	Arg	Ile	Leu	Trp	Asn
				565					570					575	
Asp	Glu	Asp	Thr	Glu	Ile	Leu	Asn	Ala	Phe	Ser	Thr	Asn	Arg	Lys	Arg
			580					585					590		
Gly	Lys	Lys	Val	Leu	Lys	Lys	Thr	Tyr	Ile	Val					
		595					600								

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<210> 50
<211> 556
<212> PRT
<213> Festuca arundinacea
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<400>	50																
Asp 1	Pro	Phe	Arg	Ala 5	Ala	Leu	Ala	Pro.	Ala 10	Ser	Pro	Pro	Leu	Glu 15	Ala		
Pro	Pro	Leu	Asp 20	Glu	Leu	Pro	Thr	Ala 25	Pro	Ser	His	Ser	Glu 30	Pro	Ala		
Ser	Ala	Ala 35	Ala	Ala	Ala	Pro	Glu 40	Gln	Asp	Pro	Val	Asp 45	Leu	Gln	His		
Glu	Glu 50	Leu	Asp	Gly	Leu	Lys 55	Ala	Gly	Val	Glu	Ala 60	Val	Arg	Ser	Arg		
Glu 65	Glu	Ser	Pro	Gln	Glu 70	Lys	Glu	Ala	Trp	Trp 75	Leu	Leu	Asn	Arg	Ala 80		
Val	Val	Asn	Tyr	Cys 85	Gly	Ser	Ala	Val	Gly 90	Thr	Val	Ala	Ala	Asn 95	Asp		
Pro	Ser	Thr	Ala 100	Asn	His	Met	Leu	Asn 105	Tyr	Asp	Gln	Val	Phe 110	Ile	Arg		
Asp	Phe	Val 115	Pro	Ser	Ala	Ile	Ala 120	Phe	Leu	Leu	Lys	Gly 125	Glu	Ser	Asp		
Ile	Val 130	Lys	Asn	Phe	Leu	Leu 135	His	Thr	Leu	Gln	Leu 140	Gln	Ser	Trp	Glu		
Lys 145	Thr	Val	Asp	Cys	Tyr 150	Ser	Pro	Gly	Gln	Gly 155	Leu	Met	Pro	Ala	Ser 160		
Phe	Lys	Val	Arg	Ser 165	Val	Pro	Leu	Asp	Gly 170	Asn	Asn	Glu	Ala	Phe 175	Glu		
Glu	Val	Leu	Asp 180	Pro	Asp	Phe	Gly	Glu 185	Ser	Ala	Ile	Gly	Arg 190	Val	Ala		
Pro	Val	Asp 195	Ser	Gly	Leu	Trp	Trp 200	Ile	Ile	Leu	Leu	Arg 205	Ala	Tyr	Gly		
Lys	Ile 210	Thr	Gly	Asp	Tyr	Ala 215	Leu	Gln	Glu	Arg	Val 220	Asp	Val	Gln	Thr		
Gly 225	Ile	Arg	Leu	Ile	Leu 230	Asn	Leu	Cys	Leu	Ser 235	Asp	Gly	Phe	Asp	Met 240		
Phe	Pro	Thr	Leu	Leu 245	Val	Thr	Asp	Gly	Ser 250	Cys	Met	Ile	Asp	Arg 255	Arg		
Met	Gly	Ile	His 260	Gly	His	Pro	Leu	Glu 265	Ile	Gln	Ala	Leu	Phe 270	Tyr	Ser		

Ala Leu Arg Cys Ala Arg Glu Met Val Asn Ile Asp Asp Gly Ser Lys  
 275 280 285  
 Asn Leu Ile Arg Val Ile Asn Asn Arg Leu Ser Ala Leu Ser Phe His  
 290 295 300  
 Ile Arg Glu Tyr Tyr Trp Val Asp Met Lys Lys Ile Asn Glu Ile Tyr  
 305 310 315 320  
 Arg Tyr Lys Thr Glu Glu Tyr Ser His Asp Ala Ile Asn Lys Phe Asn  
 325 330 335  
 Ile Tyr Pro Glu Gln Ile Pro Ser Trp Leu Ala Asp Trp Ile Pro Glu  
 340 345 350  
 Lys Gly Gly Tyr Leu Ile Gly Asn Leu Gln Pro Ala His Met Asp Phe  
 355 360 365  
 Arg Phe Phe Ser Leu Gly Asn Leu Trp Ala Ile Val Ser Ser Leu Ala  
 370 375 380  
 Thr Pro Lys Gln Ala Glu Gly Ile Leu Asn Leu Ile Glu Thr Lys Trp  
 385 390 395 400  
 Asp Asp Ile Val Ala Asn Met Pro Leu Lys Ile Cys Tyr Pro Ala Leu  
 405 410 415  
 Glu Tyr Glu Glu Trp Arg Ile Ile Thr Gly Cys Asp Pro Lys Asn Thr  
 420 425 430  
 Pro Trp Ser Tyr His Asn Gly Gly Ser Trp Pro Thr Leu Leu Trp Gln  
 435 440 445  
 Phe Thr Leu Ala Cys Ile Lys Met Gly Arg Pro Asp Leu Ala Arg Arg  
 450 455 460  
 Ala Val Glu Ala Val Glu Lys Arg Leu Ser Asp Asp Lys Trp Pro Glu  
 465 470 475 480  
 Tyr Tyr Asp Thr Arg Asn Gly Arg Phe Ile Gly Lys Gln Ser Arg Leu  
 485 490 495  
 Tyr Gln Thr Trp Thr Ile Ala Gly Phe Leu Ser Ser Lys Leu Leu Leu  
 500 505 510  
 Asp Cys Pro Glu Met Ala Ser Ile Leu Ile Cys Asp Glu Asp Leu Asp  
 515 520 525  
 Leu Leu Glu Gly Cys Ala Cys Gly Ala Asn Lys Ser Ala Arg Val Lys  
 530 535 540  
 Cys Ser Arg Arg Ala Ala Arg Ser Gln Val Leu Val  
 545 550 555

<210> 51  
 <211> 621  
 <212> PRT  
 <213> Festuca arundinacea

<400> 51  
 Met Ala Ala Ala Ile Ser His Leu Arg Arg Gly Thr Gln Arg His  
 1 5 10 15  
 Ala Leu Leu Tyr Leu Ser Arg Arg His Phe Ser Asn Ser Pro Leu Thr  
 20 25 30  
 Ala Ala Ala Pro Leu Ala Ala Ala Arg Arg Leu Leu Ser Thr Thr  
 35 40 45  
 Val Glu Ser Gly Thr Ser Ser Ala Ala Gly Ser Tyr Lys Pro Pro Pro  
 50 55 60  
 Leu Asp Pro Phe Arg Ala Ala Leu Ala Pro Ala Ser Pro Pro Leu Glu  
 65 70 75 80  
 Ser Pro Pro Leu Asp Glu Leu Pro Thr Ala Pro Ser His Ser Glu Pro  
 85 90 95  
 Ala Ser Ala Ala Ala Ala Ala Pro Glu Gln Asp Pro Val Asp Leu Gln  
 100 105 110  
 His Glu Glu Leu Asp Gly Leu Lys Ala Gly Val Glu Ala Val Arg Ser  
 115 120 125  
 Arg Glu Glu Ser Pro Gln Glu Lys Glu Ala Trp Trp Leu Leu Asn Arg  
 130 135 140  
 Ala Val Val Asn Tyr Cys Gly Ser Ala Val Gly Thr Val Ala Ala Asn  
 145 150 155 160  
 Asp Pro Ser Thr Ala Asn His Met Leu Asn Tyr Asp Gln Val Phe Ile  
 165 170 175  
 Arg Asp Phe Val Pro Ser Ala Ile Ala Phe Leu Leu Lys Gly Glu Ser  
 180 185 190  
 Asp Ile Val Lys Asn Phe Leu Leu His Thr Leu Gln Leu Gln Ser Trp

Glu Lys Thr Val Asp Cys Tyr Ser Pro Gly Gln Gly Leu Met Pro Ala  
 195 200 205  
 210 215 220  
 Ser Phe Lys Val Arg Ser Val Pro Leu Asp Gly Asn Asn Glu Ala Phe  
 225 230 235 240  
 Glu Glu Val Leu Asp Pro Asp Phe Gly Glu Ser Ala Ile Gly Arg Val  
 245 250 255  
 Ala Pro Val Asp Ser Gly Leu Trp Trp Ile Ile Leu Leu Arg Ala Tyr  
 260 265 270  
 Gly Lys Ile Thr Gly Asp Tyr Ala Leu Gln Glu Arg Val Asp Val Gln  
 275 280 285  
 Thr Gly Ile Arg Leu Ile Leu Asn Leu Cys Leu Ser Asp Gly Phe Asp  
 290 295 300  
 Met Phe Pro Thr Leu Leu Val Thr Asp Gly Ser Cys Met Ile Asp Arg  
 305 310 315 320  
 Arg Met Gly Ile His Gly His Pro Leu Glu Ile Gln Ala Leu Phe Tyr  
 325 330 335  
 Ser Ala Leu Arg Cys Ala Arg Glu Met Val Asn Ile Asp Asp Gly Ser  
 340 345 350  
 Lys Asn Leu Ile Arg Val Ile Asn Asn Arg Leu Ser Ala Leu Ser Phe  
 355 360 365  
 His Ile Arg Glu Tyr Tyr Trp Val Asp Met Lys Lys Ile Asn Glu Ile  
 370 375 380  
 Tyr Arg Tyr Lys Thr Glu Glu Tyr Ser His Asp Ala Ile Asn Lys Phe  
 385 390 395 400  
 Asn Ile Tyr Pro Glu Gln Ile Pro Ser Trp Leu Ala Asp Trp Ile Pro  
 405 410 415  
 Glu Lys Gly Gly Tyr Leu Ile Gly Asn Leu Gln Pro Ala His Met Asp  
 420 425 430  
 Phe Arg Phe Phe Ser Leu Gly Asn Leu Trp Ala Ile Val Ser Ser Leu  
 435 440 445  
 Ala Thr Pro Lys Gln Ala Glu Gly Ile Leu Asn Leu Ile Glu Thr Lys  
 450 455 460  
 Trp Asp Asp Ile Val Ala Asn Met Pro Leu Lys Ile Cys Tyr Pro Ala  
 465 470 475 480  
 Leu Glu Tyr Glu Glu Trp Arg Ile Ile Thr Gly Cys Asp Pro Lys Asn  
 485 490 495  
 Thr Pro Trp Ser Tyr His Asn Gly Gly Ser Trp Pro Thr Leu Leu Trp  
 500 505 510  
 Gln Phe Thr Leu Ala Cys Ile Lys Met Gly Arg Pro Asp Leu Ala Arg  
 515 520 525  
 Arg Ala Val Glu Ala Val Glu Lys Arg Leu Ser Asp Asp Lys Trp Pro  
 530 535 540  
 Glu Tyr Tyr Asp Thr Arg Asn Gly Arg Phe Ile Gly Lys Gln Ser Arg  
 545 550 555 560  
 Leu Tyr Gln Thr Trp Thr Ile Ala Gly Phe Leu Ser Ser Lys Leu Leu  
 565 570 575  
 Leu Asp Cys Pro Glu Met Ala Ser Ile Leu Ile Cys Asp Glu Asp Leu  
 580 585 590  
 Asp Leu Leu Glu Gly Cys Ala Cys Gly Ala Asn Lys Ser Ala Arg Val  
 595 600 605  
 Lys Cys Ser Arg Arg Ala Ala Arg Ser Gln Val Leu Val  
 610 615 620

<210> 52  
 <211> 244  
 <212> PRT  
 <213> Lolium perenne

<400> 52  
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 Glu Tyr Ser Tyr Asp Ala Val Asn Lys Phe Asn Ile Tyr Pro Asp Gln  
 20 25 30  
 Ile Pro Pro Trp Leu Val Glu Trp Ile Pro Pro Lys Gly Gly Tyr Phe  
 35 40 45  
 Ile Gly Asn Leu Gln Pro Ala His Met Asp Phe Arg Phe Phe Ser Leu  
 50 55 60

Gly Asn Leu Trp Ser Ile Val Ser Ser Leu Ala Thr Ala Asp Gln Ser  
 65 His Ala Ile Leu Asp 70 Leu Val Glu Ala Lys 75 Trp Ser Asp Leu Val 80  
 85 Lys Ile Cys Tyr Pro 90 Ala Leu Glu Asp Gln Glu Trp  
 100 Lys Phe Ile Thr Gly Ser Asp Pro 105 Lys Asn Thr Pro Trp Ser Tyr His  
 115 Asn Gly Gly Ser Trp Pro Thr Leu Leu Trp Gln Leu Thr Val Ala Cys  
 130 Ile Lys Met Asn Arg Pro 135 Glu Ile Ala Ala Arg 140 Val Glu Val Ala  
 145 Glu Ser Arg Ile Ser 150 Met Asp Lys Trp Pro 155 Glu Tyr Tyr Asp Thr Lys  
 165 Arg Gly Arg Phe Ile Gly Lys Gln Ala 170 Arg Leu Phe Gln Thr 175 Trp Ser  
 180 Ile Ala Gly Phe Leu Val Ala Lys 185 Leu Leu Leu Glu Asn Pro Glu Lys  
 195 Ser Arg Ile Leu Trp Asn Asn 200 Asp Glu Glu Ile Leu Asn Ala Leu  
 210 Ser 215 Ser Ser Pro Lys Arg 220 Lys Arg Gly Arg Lys  
 225 Thr Tyr Ile Val 230 235 240

<210> 53  
 <211> 578  
 <212> PRT  
 <213> Lolium perenne

<400> 53  
 Met Ala Ile Ala Ala Ala Ala Leu Leu Pro Leu His Leu Gly Cys  
 1 Ser Asp Ala Ala Pro Arg Arg Pro Gly Asn Ser Leu Arg Ala His Leu  
 20 Arg Lys Gly Ile Arg Gly Arg Arg Arg Ser Pro Pro Cys Ala Val  
 35 Asn Ser Leu His Pro Ser Gly Asn Pro Lys Thr Pro Gly Gly Gly Asp  
 50 Val Gly Gly Ala Trp Gly Leu Asn Gly Gly Ala Thr Ala Lys Pro Asp  
 65 His Ala Pro Pro Ser Gln Arg Arg Arg Ala Pro Arg Asp Val Glu  
 85 Glu Ala Trp Ala Leu Leu Arg Glu Ser Val Val Ser Tyr Cys Gly Ser  
 100 Pro Val Gly Thr Ile Ala Ala Cys Asp Pro Asn Asp Ala Ser Pro Leu  
 115 Asn Tyr Asp Gln Val Phe Ile Arg Asp Phe Val Pro Ser Gly Val Ala  
 130 Phe Leu Leu Lys Gly Glu His Glu Ile Val Arg Asn Phe Ile Leu His  
 145 Thr Leu Gln Leu Gln Ser Trp Glu Lys Thr Ile Asp Cys His Ser Pro  
 165 Gly Gln Gly Leu Met Pro Ala Ser Phe 170 Lys Val Arg Val Val Pro Leu  
 180 Asp Gly Gly Asp Asp Gly Ala Thr Glu Glu Val Leu Asp Pro Asp Phe  
 195 Gly Glu Ala Ala Ile Gly Arg Val Ala Pro Val Asp Ser Gly Leu Trp  
 210 Trp Ile Ile Leu Leu Arg Ala Tyr Gly Lys Cys Ser Gly Asp Leu Ser  
 225 Phe His Glu Arg Val 230 Asp Val Gln Thr Gly Ile Lys Leu Ile Leu Lys  
 245 Leu Cys Leu Ala Asp Gly Phe Asp Met Phe Pro Thr Leu Leu Val Thr  
 260 Asp Gly Ser Cys Met Met Asp Arg Arg Met Gly Ile His Gly His Pro  
 275 Leu Glu Ile Gln Ala Leu Phe Tyr Ser Ala Leu Leu Ser Ala Arg Glu

290 295 300  
 Met Leu Thr Pro Glu Asp Gly Ser Ala Asp Leu Ile Arg Ala Leu Asn  
 305 310 315 320  
 Ser Arg Leu Met Ala Leu Ser Phe His Ile Arg Glu Tyr Tyr Trp Leu  
 325 330 335  
 Glu Lys Arg Lys Leu Asn Glu Ile Tyr Arg Tyr Lys Thr Glu Glu Tyr  
 340 345 350  
 Ser Tyr Asp Ala Val Asn Lys Phe Asn Ile Tyr Pro Asp Gln Ile Pro  
 355 360 365  
 Pro Trp Leu Val Glu Trp Ile Pro Pro Lys Gly Gly Tyr Phe Ile Gly  
 370 375 380  
 Asn Leu Gln Pro Ala His Met Asp Phe Arg Phe Ser Leu Gly Asn  
 385 390 395 400  
 Leu Trp Ser Ile Val Ser Ser Leu Ala Thr Ala Asp Gln Ser His Ala  
 405 410 415  
 Ile Leu Asp Leu Val Glu Ala Lys Trp Ser Asp Leu Val Ala Glu Met  
 420 425 430  
 Pro Met Lys Ile Cys Tyr Pro Ala Leu Glu Asp Gln Glu Trp Lys Phe  
 435 440 445  
 Ile Thr Gly Ser Asp Pro Lys Asn Thr Pro Trp Ser Tyr His Asn Gly  
 450 455 460  
 Gly Ser Trp Pro Thr Leu Trp Gln Leu Thr Val Ala Cys Ile Lys  
 465 470 475 480  
 Met Asn Arg Pro Glu Ile Ala Ala Arg Ala Val Glu Val Ala Glu Ser  
 485 490 495  
 Arg Ile Ser Met Asp Lys Trp Pro Glu Tyr Tyr Asp Thr Lys Arg Gly  
 500 505 510  
 Arg Phe Ile Gly Lys Gln Ala Arg Leu Phe Gln Thr Trp Ser Ile Ala  
 515 520 525  
 Gly Phe Leu Val Ala Lys Leu Leu Glu Asn Pro Glu Lys Ser Arg  
 530 535 540  
 Ile Leu Trp Asn Asn Glu Asp Glu Glu Ile Leu Asn Ala Leu Ser Leu  
 545 550 555 560  
 Met Thr Gly Pro Ser Ser Pro Lys Arg Lys Arg Gly Arg Lys Thr Tyr  
 565 570 575  
 Ile Val

<210> 54  
 <211> 619  
 <212> PRT  
 <213> Lolium perenne

<400> 54  
 Met Asn Gly Gln Thr Thr Met Gly Leu Ala Ala Ala Ala Ala Ala Ala  
 1 5 10 15  
 Val Arg Pro Cys Arg Arg Arg Leu Leu Ser Ser Ala Ser Ala Ala Ala  
 20 25 30  
 Ala Ala Lys Ala Ser Ala Thr Pro Leu Phe Pro Arg Cys Ser His Pro  
 35 40 45  
 Gln His Gln Gln His Ser Arg Arg Ile Pro Phe Leu Val Ser Ala Ala  
 50 55 60  
 Ser His Thr Ser Gln Ser Asp Pro Ser Thr Thr Pro Thr Pro Val Thr  
 65 70 75 80  
 Ser Asp Pro Arg Ser Ala Val Ala Gly Asn Leu Pro Phe Phe Asp Arg  
 85 90 95  
 Val Leu Phe Pro Gly Ser Phe Pro Leu Glu Thr Pro Pro Val Glu Glu  
 100 105 110  
 Pro Ala Pro Ala Pro Pro Ala Asp Glu Ala Gln Ala Ser Ala Ser Pro  
 115 120 125  
 Val Arg Glu Glu Ser Asp Thr Glu Arg Glu Ala Trp Arg Leu Leu Arg  
 130 135 140  
 Arg Ala Val Val Ser Tyr Cys Gly Asp Pro Val Gly Thr Val Ala Ala  
 145 150 155 160  
 Glu Asp Pro Glu Cys Thr Glu Met Leu Asn Tyr Asp Gln Val Phe Ile  
 165 170 175  
 Arg Asp Phe Val Pro Ser Ala Leu Ala Phe Leu Met Arg Gly Glu Thr  
 180 185 190

Glu Ile Val Arg Asn Phe Leu Leu His Thr Leu Gln Leu Gln Ser Trp  
 195 200 205  
 Glu Lys Thr Val Asp Cys Tyr Ser Pro Gly Gln Gly Leu Met Pro Ala  
 210 215 220  
 Ser Phe Lys Ile Lys Thr Val Pro Leu Asp Glu Asn Asn Glu Ala Phe  
 225 230 235 240  
 Glu Glu Val Leu Asp Pro Asp Phe Gly Ser Ala Ile Gly Arg Val  
 245 250 255  
 Ala Pro Val Asp Ser Gly Leu Trp Trp Ile Ile Leu Leu Arg Ala Tyr  
 260 265 270  
 Cys Lys Phe Thr Gly Asp Tyr Ser Leu Gln Glu Arg Val Asp Val Gln  
 275 280 285  
 Thr Gly Ile Lys Leu Ile Leu Ser Leu Cys Leu Thr Asp Gly Phe Asp  
 290 295 300  
 Met Phe Pro Thr Leu Leu Val Thr Asp Gly Ser Cys Met Ile Asp Arg  
 305 310 315 320  
 Arg Met Gly Ile His Gly His Pro Leu Glu Ile Gln Ala Leu Phe Tyr  
 325 330 335  
 Ser Ala Leu Arg Cys Ser Arg Glu Met Ile Val Met Asn Asp Gly Ser  
 340 345 350  
 Lys His Leu Leu Gln Ala Ile Asn Asn Arg Leu Ser Ala Leu Ser Phe  
 355 360 365  
 His Ile Arg Glu Tyr Tyr Trp Val Asp Met Lys Lys Ile Asn Glu Ile  
 370 375 380  
 Tyr Arg Tyr Lys Thr Glu Glu Tyr Ser His Asp Ala Thr Asn Lys Phe  
 385 390 395 400  
 Asn Ile Tyr Pro Glu Gln Ile Pro Ser Trp Leu Val Asp Trp Val Pro  
 405 410 415  
 Glu Lys Gly Gly Tyr Leu Ile Gly Asn Leu Gln Pro Ala His Met Asp  
 420 425 430  
 Phe Arg Phe Phe Ser Leu Gly Asn Leu Trp Ala Ile Ser Ser Ser Leu  
 435 440 445  
 Thr Thr Pro Thr Gln Ala Glu Gly Ile Leu Ser Leu Ile Glu Glu Lys  
 450 455 460  
 Trp Asp Asp Leu Val Ala Asn Met Pro Leu Lys Ile Cys Tyr Pro Ala  
 465 470 475 480  
 Met Glu Asp Asp Glu Trp Arg Ile Val Thr Gly Ser Asp Pro Lys Asn  
 485 490 495  
 Thr Pro Trp Ser Tyr His Asn Gly Gly Ser Trp Pro Thr Leu Trp  
 500 505 510  
 Gln Phe Thr Leu Ala Cys Ile Lys Met Gly Arg Pro Glu Leu Ala Arg  
 515 520 525  
 Arg Ala Ile Ala Val Ala Glu Lys Leu Ser Ala Asp Lys Trp Pro  
 530 535 540  
 Glu Tyr Tyr Asp Thr Arg Ser Gly Arg Phe Val Gly Lys Gln Ser Arg  
 545 550 555 560  
 Ser Tyr Gln Thr Trp Thr Ile Ala Gly Phe Leu Thr Ser Lys Ile Leu  
 565 570 575  
 Leu Glu Asn Pro Glu Leu Ala Ser Ile Leu Thr Cys Asp Glu Asp Leu  
 580 585 590  
 Glu Leu Leu Glu Gly Cys Ala Cys Cys Leu Ser Lys Arg Thr Arg Cys  
 595 600 605  
 Ser Arg Arg Val Thr Lys Ser Asp Ile Ile Gly  
 610 615

<210> 55  
 <211> 578  
 <212> PRT  
 <213> Lolium perenne

<400> 55  
 Met Ala Ile Ala Ala Ala Ala Leu Leu Pro Leu His Leu Gly Cys  
 1 5 10 15  
 Ser Asp Ala Ala Pro Arg Arg Pro Gly Asn Ser Leu Arg Ala His Leu  
 20 25 30  
 Arg Lys Gly Gly Ile Arg Gly Arg Arg Ser Pro Pro Cys Ala Val  
 35 40 45  
 Asn Ser Leu His Pro Ser Gly Asn Pro Lys Thr Pro Gly Gly Gly Asp



Val	50	Gly	Gly	Gly	Arg	Gly	55	Val	Asn	Gly	Gly	Ala	60	Thr	Ala	Lys	Pro	Asp
65	His	Ala	Pro	Pro	Ser	70	Gln	Arg	Arg	Arg	Ala	75	Pro	Arg	Asp	Val	Glu	80
Glu	Ala	Trp	Ala	Leu	Leu	Arg	Glu	Ser	105	Val	Val	Ser	Tyr	Cys	Gly	Ser		
Pro	Val	Gly	100	Thr	Ile	Ala	Ala	Cys	120	Asp	Pro	Asn	Asp	Ala	Ser	Pro	Leu	
Asn	Tyr	115	Asp	Gln	Val	Phe	Ile	Arg	Asp	Phe	Val	Pro	Ser	Gly	Val	Ala		
130	Phe	Leu	Leu	Lys	Gly	Glu	135	His	Glu	Ile	Val	Arg	140	Asn	Phe	Ile	Leu	His
145	Thr	Leu	Gln	Leu	Gln	Ser	Trp	Glu	Lys	Thr	Ile	Asp	155	Cys	His	Ser	Pro	160
Gly	Gln	Gly	165	Met	Pro	Ala	Ser	Phe	170	Lys	Val	Arg	175	Val	Val	Pro	Leu	
Asp	Gly	Gly	180	Asp	Asp	Gly	Ala	Thr	185	Glu	Glu	Val	Leu	Asp	Pro	Asp	Phe	
Gly	Glu	Ala	195	Ala	Ile	Gly	Arg	Val	200	Ala	Pro	Val	Asp	Ser	Gly	Leu	Trp	
Trp	Ile	Ile	Leu	Leu	Arg	Ala	Tyr	Gly	210	Lys	Cys	Ser	Gly	Asp	Leu	Ser		
225	Phe	His	Glu	Arg	Val	Asp	Val	Gln	215	Thr	Gly	Ile	Lys	Leu	Ile	Leu	Lys	
Leu	Cys	Leu	Ala	Asp	Gly	Phe	Asp	Met	230	Phe	Pro	Thr	Leu	Leu	Val	Thr		
Asp	Gly	Ser	245	Cys	Met	Met	Asp	Arg	245	Met	Gly	Ile	His	Gly	His	Pro		
Leu	Glu	Ile	Gln	Ala	Leu	Phe	250	Tyr	255	Ser	Ala	Leu	Leu	Ser	Ala	Arg	Glu	
Met	Leu	Thr	Pro	Glu	Asp	Gly	260	Ser	265	Ala	Asp	Leu	Ile	Arg	Ala	Leu	Asn	
305	Ser	Arg	Leu	Met	Ala	Leu	Ser	Phe	270	His	Ile	Arg	Glu	Tyr	Tyr	Trp	Leu	
Glu	Lys	Arg	Lys	Leu	Asn	Glu	Ile	Tyr	275	Arg	Tyr	Lys	Thr	Glu	Gln	Ile	Pro	
Ser	Tyr	Asp	Ala	Val	Asn	Lys	Phe	Asn	280	Ile	Tyr	Pro	Asp	Gln	Ile	Pro		
Pro	Trp	Leu	Val	Glu	Trp	Ile	300	Pro	305	Lys	Gly	Gly	Tyr	Phe	Ile	Gly		
Asn	Leu	Gln	Pro	Ala	His	Met	310	Asp	315	Phe	Arg	Phe	Ser	Leu	Gly	Asn		
385	Leu	Trp	Ser	Ile	Val	Ser	315	Leu	320	Ala	Thr	Ala	Asp	Gln	Ser	His	Ala	
Ile	Leu	Asp	Leu	Val	Glu	Ala	Lys	Trp	325	Ser	Asp	Leu	Val	Ala	Glu	Met		
Pro	Met	Lys	Ile	Cys	Tyr	Pro	Ala	Leu	330	Glu	Asp	Gln	Glu	Trp	Lys	Phe		
Ile	Thr	Gly	Ser	Asp	Pro	Lys	400	Asn	405	Thr	Pro	Trp	Ser	Tyr	His	Asn	Gly	
Gly	Ser	Trp	Pro	Thr	Leu	Leu	410	Trp	415	Gln	Leu	Thr	Val	Ala	Cys	Ile	Lys	
465	Met	Asn	Arg	Pro	Glu	Ile	420	Ala	425	Ala	Arg	Ala	Val	Ala	Glu	Ser		
Arg	Ile	Ser	Thr	Asp	Lys	Trp	430	Pro	435	Glu	Tyr	Tyr	Asp	Thr	Lys	Arg	Gly	
Arg	Phe	Ile	Gly	Lys	Gln	Ala	440	Arg	445	Leu	Phe	Gln	Thr	Trp	Ser	Ile	Ala	
Gly	Phe	Leu	Val	Ala	Lys	Leu	450	Leu	455	Leu	Glu	Asn	Pro	Glu	Lys	Ser	Arg	
Ile	Leu	Trp	Asn	Asn	Glu	Asp	460	Glu	465	Glu	Ile	Leu	Asn	Ala	Leu	Ser	Leu	
545	Met	Thr	Gly	Pro	Ser	Ser	470	Pro	475	Lys	Arg	Gly	Arg	Lys	Thr	Tyr		
Ile	Val																	

<210> 56  
 <211> 554  
 <212> PRT  
 <213> *Lolium perenne*

<400> 56  
 Met Lys Arg Val Ser Ser His Val Ser Ile Ala Ser Glu Ala Glu Ile  
 1 5 10 15  
 Asn Leu Asp Leu Ser Arg Leu Leu Ile Asp Lys Pro Arg Tyr Thr Leu  
 20 25 30  
 Glu Arg Lys Arg Ser Phe Asp Glu Gln Ser Trp Ser Glu Leu Thr His  
 35 40 45  
 Thr His Arg Gln Asn Asp Gly Phe Asp Ser Val Leu Gln Ser Pro Ala  
 50 55 60  
 Phe Arg Thr Gly Phe Asp Ser Pro Phe Ser Met Gly Thr His Phe Gly  
 65 70 75 80  
 Glu Pro Ser Gly Pro His Pro Leu Val Asn Glu Ala Trp Glu Ala Leu  
 85 90 95  
 Arg Lys Ser Val Tyr Phe Arg Gly Gln Pro Val Gly Thr Ile Ala  
 100 105 110  
 Ala Val Asp His Ala Ser Glu Glu Val Leu Asn Tyr Asp Gln Val Phe  
 115 120 125  
 Val Arg Asp Phe Val Pro Ser Ala Leu Ala Phe Leu Met Asn Asn Glu  
 130 135 140  
 Pro Glu Ile Val Lys Asn Phe Leu Leu Lys Thr Leu His Leu Gln Ser  
 145 150 155 160  
 Ser Glu Lys Met Val Asp Arg Phe Lys Leu Gly Ala Gly Ala Met Pro  
 165 170 175  
 Ala Ser Phe Lys Val Asp Arg Asn Lys Ser Arg Asn Thr Glu Thr Leu  
 180 185 190  
 Val Ala Asp Phe Gly Glu Ser Ala Ile Gly Arg Val Ala Pro Val Asp  
 195 200 205  
 Ser Gly Phe Trp Trp Ile Ile Leu Leu Arg Ala Tyr Thr Lys Tyr Thr  
 210 215 220  
 Gly Asp Ala Ser Leu Ser Glu Ser Pro Asp Cys Gln Lys Cys Met Arg  
 225 230 235 240  
 Leu Ile Leu Asn Leu Cys Leu Ser Glu Gly Phe Asp Thr Phe Pro Thr  
 245 250 255  
 Leu Leu Cys Thr Asp Gly Cys Ser Met Ile Asp Arg Arg Met Gly Ile  
 260 265 270  
 Tyr Gly Tyr Pro Ile Glu Ile Gln Ala Leu Phe Tyr Met Ala Leu Arg  
 275 280 285  
 Cys Ala Leu Gln Met Leu Lys Pro Asp Gly Glu Gly Lys Asp Phe Ile  
 290 295 300  
 Glu Lys Ile Gly Gln Arg Leu His Ala Leu Thr Tyr His Met Arg Asn  
 305 310 315 320  
 Tyr Phe Trp Leu Asp Phe Pro His Leu Asn Ile Tyr Arg Tyr Lys  
 325 330 335  
 Thr Glu Glu Tyr Ser His Thr Ala Val Asn Lys Phe Asn Val Ile Pro  
 340 345 350  
 Asp Ser Ile Pro Asp Trp Val Phe Asp Phe Met Pro Cys Arg Gly Gly  
 355 360 365  
 Tyr Phe Leu Gly Asn Val Ser Pro Ala Met Met Asp Phe Arg Trp Phe  
 370 375 380  
 Ala Leu Gly Asn Cys Ile Ala Ile Ile Ser Ser Leu Ala Thr Pro Glu  
 385 390 395 400  
 Gln Ser Ser Ala Ile Met Asp Leu Ile Glu Glu Arg Trp Asp Glu Leu  
 405 410 415  
 Val Gly Glu Val Pro Leu Lys Ile Cys Tyr Pro Ala Ile Glu Asn His  
 420 425 430  
 Glu Trp Arg Ile Ile Thr Gly Cys Asp Pro Lys Asn Thr Arg Trp Ser  
 435 440 445  
 Tyr His Asn Gly Gly Ser Trp Pro Val Leu Leu Trp Leu Leu Thr Ala  
 450 455 460  
 Ala Cys Ile Lys Thr Gly Arg Pro Gln Met Ala Lys Arg Ala Ile Glu  
 465 470 475 480  
 Leu Ser Glu Ala Arg Leu Leu Lys Asp Gly Trp Pro Glu Tyr Tyr Asp  
 485 490 495

Gly Lys Leu Gly Lys Phe Val Gly Lys Gln Ala Arg Lys Phe Gln Thr  
 500 505 510  
 Trp Ser Ile Ala Gly Tyr Leu Val Ala Arg Met Met Leu Glu Asp Pro  
 515 520 525  
 Ser Thr Leu Met Met Ile Ser Met Glu Glu Asp Arg Pro Val Lys Pro  
 530 535 540  
 Thr Met Arg Arg Ser Ala Ser Trp Asn Ala  
 545 550

<210> 57  
 <211> 552  
 <212> PRT  
 <213> Lolium perenne

<400> 57  
 Met Glu Ala Pro Gly Gly Gly Ala Gly Pro Met Pro Thr Thr Pro Ser  
 1 5 10 15  
 His Ala Ser Ile Ala Asp Ser Asp Phe Asp Leu Ser Arg Leu Leu  
 20 25 30  
 Asn His Arg Pro Arg Ile Asn Val Glu Arg Gln Arg Ser Phe Asp Asp  
 35 40 45  
 Arg Ser Leu Gly Asp Leu Tyr Leu Ser Ala Met Asp Ser Arg Gly Gly  
 50 55 60  
 Tyr Met Asp Ser Tyr Asp Ser Met Tyr Ser Pro Gly Gly Gly Leu Arg  
 65 70 75 80  
 Ser Leu Thr Gly Thr Pro Ala Ser Ser Thr Arg Leu Ser Phe Glu Pro  
 85 90 95  
 Gln Leu Leu Val Ala Glu Ala Trp Glu Ala Leu Arg Arg Ser Leu Val  
 100 105 110  
 Cys Phe Arg Gly Glu Pro Leu Gly Thr Ile Ala Ala Val Asp Ser Ser  
 115 120 125  
 Ser Asp Glu Val Leu Asn Tyr Asp Gln Val Phe Val Arg Asp Phe Val  
 130 135 140  
 Pro Ser Ala Leu Ala Phe Leu Met Asn Gly Glu Pro Asp Ile Val Lys  
 145 150 155 160  
 Asn Phe Leu Leu Thr Leu Leu Leu Gln Gly Trp Glu Lys Arg Ile  
 165 170 175  
 Asp Arg Phe Lys Leu Gly Glu Gly Ala Met Pro Ala Ser Phe Lys Val  
 180 185 190  
 Leu Lys Asp Pro Lys Arg Gly Val Asp Thr Leu Ala Ala Asp Phe Gly  
 195 200 205  
 Glu Ser Ala Ile Gly Arg Val Ala Pro Ala Asp Ser Gly Phe Trp Trp  
 210 215 220  
 Ile Ile Leu Leu Arg Ala Tyr Thr Lys Ser Thr Gly Asp Leu Thr Leu  
 225 230 235 240  
 Ala Glu Thr Pro Glu Cys Gln Lys Gly Ile Arg Leu Ile Met Asn Gln  
 245 250 255  
 Cys Leu Ala Glu Gly Phe Asp Thr Phe Pro Thr Leu Leu Cys Ala Asp  
 260 265 270  
 Gly Cys Cys Met Ile Asp Arg Arg Met Gly Val Tyr Gly Tyr Pro Ile  
 275 280 285  
 Glu Ile Gln Ala Leu Phe Phe Met Ser Leu Arg Cys Ala Leu Leu Leu  
 290 295 300  
 Leu Lys Pro Ala Val Glu Gly Asn Ser Ser Ser Lys Asp Asp Asp Ile  
 305 310 315 320  
 Met Glu Arg Ile Val Thr Arg Leu His Ala Leu Ser Tyr His Met Arg  
 325 330 335  
 Ser Tyr Phe Trp Leu Asp Phe Gln Gln Leu Asn Val Ile Tyr Arg Phe  
 340 345 350  
 Lys Thr Glu Glu Tyr Ser His Thr Ala Val Asn Lys Phe Asn Val Ile  
 355 360 365  
 Pro Glu Ser Ile Pro Asp Trp Leu Phe Asp Phe Met Pro Ser Arg Gly  
 370 375 380  
 Gly Tyr Phe Val Gly Asn Val Ser Pro Ala Arg Met Asp Phe Arg Trp  
 385 390 395 400  
 Phe Ala Leu Gly Asn Cys Val Ala Ile Leu Ala Ser Leu Ala Thr Pro  
 405 410 415  
 Glu Gln Ala Gly Ala Ile Met Asp Leu Ile Glu Glu Arg Trp Glu Asp

Leu Ile Gly 420 Glu Met Pro Leu Lys 425 Ile Cys Tyr Pro Thr 430 Ile Glu Gly  
 His Glu 435 Trp Gln Asn Val Thr 440 Gly Cys Asp Pro Lys 445 Asn Thr Arg Trp  
 Ser Tyr His Asn Gly Gly Ser Trp Pro Val Leu 460 Ile Trp Leu Leu Thr 480  
 Ala Ala Cys Ile Lys 470 Thr Gly Arg Leu Lys 475 Ile Ala Arg Arg Ala Ile  
 Asp Leu Ala Glu 485 Ala Arg Leu Gly Lys 490 Asp Gly Trp Pro Glu Tyr Tyr  
 Asp Gly Lys 500 Leu Gly Arg Tyr Val 505 Gly Lys Gln Ala Arg Lys His Gln  
 Thr Trp Ser 515 Ile Ala Gly Tyr 520 Leu Val Ala Lys Met 525 Met Leu Glu Asp  
 Pro Ser His Leu Gly Met 535 Ile Ser  
 545 550

&lt;210&gt; 58

&lt;211&gt; 562

&lt;212&gt; PRT

&lt;213&gt; Lolium perenne

&lt;400&gt; 58

Met Glu Phe Gly Ala Pro Gly Gly Met Arg Arg Ser Ala Ser His Asn  
 1 5 10 15  
 Ser Leu Ser Gly Ser Asp Asp Phe Asp Leu Thr His Leu Leu Asn Lys  
 20 25 30  
 Pro Arg Ile Asn Val Glu Arg Gln Arg Ser Phe Asp Asp Arg Ser Leu  
 35 40 45  
 Ser Asp Val Ser Tyr Ser Gly Gly Gly His Ala Arg Gly Ala Gly Gly  
 50 55 60  
 Gly Phe Asp Gly Met Tyr Ser Pro Gly Gly Gly Leu Arg Ser Leu Val  
 65 70 75 80  
 Gly Thr Pro Ala Ser Ser Ala Leu His Ser Phe Glu Pro His Pro Ile  
 85 90 95  
 Val Gly Asp Ala Trp Glu Ala Leu Arg Arg Ser Leu Val Phe Phe Arg  
 100 105 110  
 Gly Gln Pro Leu Gly Thr Ile Ala Ala Tyr Asp His Ala Ser Glu Glu  
 115 120 125  
 Val Leu Asn Tyr Asp Gln Val Phe Val Arg Asp Phe Val Pro Ser Ala  
 130 135 140  
 Met Ala Phe Leu Met Asn Gly Glu Pro Glu Ile Val Lys Asn Phe Leu  
 145 150 155 160  
 Leu Lys Thr Val Leu Leu Gln Gly Trp Glu Lys Lys Val Asp Arg Phe  
 165 170 175  
 Lys Leu Gly Glu Gly Ala Met Pro Ala Ser Phe Lys Val Leu His Asp  
 180 185 190  
 Asp Lys Lys Gly Val Asp Thr Leu His Ala Asp Phe Gly Glu Ser Ala  
 195 200 205  
 Ile Gly Arg Val Ala Pro Val Asp Ser Gly Phe Trp Trp Ile Ile Leu  
 210 215 220  
 Leu Arg Ala Tyr Thr Lys Ser Thr Gly Asp Leu Thr Leu Ala Glu Lys  
 225 230 235 240  
 Pro Glu Cys Gln Lys Ala Met Arg Leu Ile Leu Ser Leu Cys Leu Ser  
 245 250 255  
 Glu Gly Phe Asp Thr Phe Pro Thr Leu Cys Ala Asp Gly Cys Cys  
 260 265 270  
 Met Ile Asp Arg Arg Met Gly Val Tyr Gly Tyr Pro Ile Glu Ile Gln  
 275 280 285  
 Ser Leu Phe Phe Met Ala Leu Arg Cys Ala Leu Leu Met Leu Lys His  
 290 295 300  
 Asp Asn Glu Gly Lys Asp Phe Val Glu Arg Ile Ala Thr Arg Leu His  
 305 310 315 320  
 Ala Leu Ser Tyr His Met Arg Ser Tyr Phe Trp Leu Asp Phe Gln Gln  
 325 330 335  
 Leu Asn Asp Ile Tyr Arg Tyr Lys Thr Glu Glu Tyr Ser His Thr Ala  
 340 345 350

Val Asn Lys Phe Asn Val Ile Pro Asp Ser Ile Pro Asp Trp Leu Phe  
 355 360 365  
 Asp Phe Met Pro Cys Glu Gly Gly Phe Phe Val Gly Asn Val Ser Pro  
 370 375 380  
 Ala Arg Met Asp Phe Arg Trp Phe Ala Leu Gly Asn Met Ile Ala Ile  
 385 390 395 400  
 Val Ser Ser Leu Ala Thr Pro Glu Gln Ser Thr Ala Ile Met Asp Leu  
 405 410 415  
 Ile Glu Glu Arg Trp Glu Glu Leu Ile Gly Glu Met Pro Leu Lys Ile  
 420 425 430  
 Cys Tyr Pro Ala Ile Glu Asn His Glu Trp Arg Ile Val Thr Gly Cys  
 435 440 445  
 Asp Pro Lys Asn Thr Arg Trp Ser Tyr His Asn Gly Gly Ser Trp Pro  
 450 455 460  
 Val Leu Leu Trp Leu Leu Thr Ala Ala Ser Ile Lys Thr Gly Arg Pro  
 465 470 475 480  
 Gln Ile Ala Arg Arg Ala Ile Asp Leu Ala Glu Arg Arg Leu Leu Lys  
 485 490 495  
 Asp Gly Trp Pro Glu Tyr Tyr Asp Gly Lys Leu Gly Lys Tyr Val Gly  
 500 505 510  
 Lys Gln Ala Arg Lys Phe Gln Thr Trp Ser Ile Ala Gly Tyr Leu Val  
 515 520 525  
 Ala Lys Met Leu Leu Glu Asp Pro Ser His Leu Gly Met Ile Ala Leu  
 530 535 540  
 Glu Glu Asp Lys Ala Met Lys Pro Val Leu Arg Arg Ser Ala Ser Trp  
 545 550 555 560  
 Thr Asn

<210> 59  
 <211> 616  
 <212> PRT  
 <213> Lolium perenne

<400> 59  
 Met Asp Ser Asp Tyr Gly Val Pro Arg Glu Leu Ser Glu Val Gln Lys  
 1 5 10 15  
 Lys Arg Thr Leu Tyr Gln Pro Asp Leu Pro Pro Cys Leu Gln Gly Thr  
 20 25 30  
 Thr Val Arg Val Glu Tyr Gly Asp Val Ala Ile Ala Asp Pro Ala  
 35 40 45  
 Gly Ala His Val Ile Ser His Ala Phe Pro His Thr Tyr Gly Gln Pro  
 50 55 60  
 Leu Ala His Phe Leu Arg Lys Ala Ala Asn Val Ala Asp Ala Lys Val  
 65 70 75 80  
 Ile Ser Glu His Pro Ala Val Arg Val Ile Val Phe Cys Gly Arg  
 85 90 95  
 Gln Ser Pro Gly Gly His Asn Val Ile Trp Gly Leu His Asp Ala Ile  
 100 105 110  
 Lys Ala His Asn Pro Asn Ser Lys Leu Ile Gly Phe Leu Gly Gly Ser  
 115 120 125  
 Asp Gly Leu Leu Ala Gln Lys Thr Leu Glu Ile Thr Asp Glu Val Leu  
 130 135 140  
 Ser Ser Tyr Lys Asn Gln Gly Gly Tyr Asp Met Leu Gly Arg Thr Lys  
 145 150 155 160  
 Asp Gln Ile Arg Thr Thr Glu Gln Val Asn Gly Ala Met Ala Ser Cys  
 165 170 175  
 Gln Ala Leu Lys Leu Asp Ala Leu Ile Ile Ile Gly Gly Val Thr Ser  
 180 185 190  
 Asn Thr Asp Ala Ala Gln Leu Ala Glu Thr Phe Ala Glu Ala Lys Cys  
 195 200 205  
 Ala Thr Lys Val Val Gly Val Pro Val Thr Leu Asn Gly Asp Leu Lys  
 210 215 220  
 Asn Gln Phe Val Glu Thr Thr Val Gly Phe Asp Thr Ile Cys Lys Val  
 225 230 235 240  
 Asn Ser Gln Leu Ile Ser Asn Met Cys Thr Asp Ala Leu Ser Ala Glu  
 245 250 255  
 Lys Tyr Tyr Tyr Phe Ile Arg Met Met Gly Arg Lys Ala Ser His Val

Ala Leu Glu 260 Cys Ala Leu Gln Ser 265 His Pro Asn Met Val 270 Ile Leu Gly  
 Glu Glu 275 Val Ala Ala Ser Lys 280 Leu Thr Ile Phe Asp 285 Ile Thr Lys Gln  
 Ile Cys Asp 290 Ala Val Gln Ala Arg Ala Glu Lys 300 Asp Lys Asn His Gly  
 Val 305 Ile Leu Ile Pro 310 Glu Gly Leu Val Glu Ser 315 Ile Pro Glu Leu Tyr  
 Ala Leu Leu Gln 325 Glu Ile Asn Gly Leu His Gly Lys Gly Val 335 Ser Ile  
 Glu Asn Ile 340 Ser Ser Gln Leu Ser 345 Pro Trp Ala Ser Ala Leu Phe Glu  
 Phe Leu 355 Pro Gln Phe Ile Arg 360 Gln Gln Leu Leu Leu Arg Pro Glu Ser  
 Asp 370 Asp Ser Ala Gln Leu Ser Gln Ile Glu Thr 380 Glu Lys Leu Leu Ala  
 Gln 385 Leu Val Glu Thr 390 Glu Met Asn Lys Arg 395 Leu Lys Glu Gly Thr Tyr  
 Lys Gly Lys Lys 405 Phe Asn Ala Ile Cys 410 His Phe Phe Gly Tyr Gln Ala  
 Arg Gly Ala Met Pro Ser Lys Phe 425 Asp Cys Asp Tyr Ala Tyr Val Leu  
 Gly His Val Ser Tyr His Ile 435 Leu Ala Ala Gly Leu Asn Gly Tyr Met  
 Ala Thr Val Thr Asn Leu Lys Ser Pro Leu Asn Lys Trp Arg Cys Gly  
 Ala 465 Ala Pro Ile Ser 470 Ser Met Met Thr Val Lys Arg Trp Ser Arg Gly  
 Pro Ser Thr Thr 485 Gln Ile Gly Lys Pro Ala Val His Met Ala Ser Val  
 Asp Leu Arg Gly Lys Ala Tyr Glu 500 Leu Leu Arg Gln Asn 510 Ser Ser Ser  
 Cys Leu Leu Glu Asp Ile Tyr Arg Asn Pro Gly Pro Leu Gln Phe Glu  
 Gly 530 Pro Gly Ser Asp Ser Lys Pro Ile Ser Leu Cys Val Glu Asp Gln  
 Asp 545 Tyr Met Gly Arg Ile Lys Lys Leu Gln Glu Tyr Leu Glu Lys Val  
 Lys Ser Ile Val Lys Pro Gly Cys Ser 570 Gln Asp Val Leu Lys Ala Ala  
 Leu Ser Ala Met Ser Ser Val Thr 585 Asp Thr Leu Ala Ile Met Thr Ser  
 Ser 595 Thr Gly Gln Ala Pro 600 Leu  
 Ser 610

&lt;210&gt; 60

&lt;211&gt; 616

&lt;212&gt; PRT

&lt;213&gt; Festuca arundinacea

&lt;400&gt; 60

Met Asp Ser Asp Tyr Gly Val Pro Arg Glu Leu Ser Glu Val Gln Lys  
 1 Lys Arg Thr Leu Tyr Gln Pro Glu Leu Pro Pro Cys Leu Gln Gly Thr  
 Thr Val Arg Val Glu Tyr Gly Asp 25 Val Ala Ile Ala Ala Asp Pro Ala  
 Gly Ala His Val Ile Ser His Ala Phe Pro His Thr Tyr Gly Gln Pro  
 50 Leu Ala His Phe Leu Arg Lys Ala Ala Asn Val Ala Asp Ala Lys Val  
 65 Ile Ser Glu His Pro Ala Val Arg Val Gly Ile Val Phe Cys Gly Arg  
 Gln Ser Pro Gly 85 Gly His Asn Val Ile 90 Trp Gly Leu His Asp Ala Ile  
 Lys Ala His Asn Ser Asn Ser Lys 105 Leu Ile Gly Phe Leu Gly Gly Ser  
 115

Asp Gly Leu Leu Ala Gln Lys Thr Leu Glu Ile Thr Asp Glu Val Leu  
 130 135 140  
 Ser Ser Tyr Lys Asn Gln Gly Gly Tyr Asp Met Leu Gly Arg Thr Lys  
 145 150 155  
 Asp Gln Ile Arg Thr Thr Glu Gln Val Asn Gly Ala Met Ala Ser Cys  
 165 170 175  
 Gln Asp Leu Lys Leu Asp Ala Leu Ile Ile Gly Gly Val Thr Ser  
 180 185 190  
 Asn Thr Asp Ala Ala Gln Leu Ala Glu Thr Phe Ala Glu Ala Lys Cys  
 195 200 205  
 Ala Thr Lys Val Val Gly Val Pro Val Thr Leu Asn Gly Asp Leu Lys  
 210 215 220  
 Asn Gln Phe Val Glu Thr Thr Val Gly Phe Asp Thr Ile Cys Lys Val  
 225 230 235  
 Asn Ser Gln Leu Ile Ser Asn Met Cys Thr Asp Ala Leu Ser Ala Glu  
 245 250 255  
 Lys Tyr Tyr Tyr Phe Ile Arg Met Met Gly Arg Lys Ala Ser His Val  
 260 265 270  
 Ala Leu Glu Cys Ala Leu Gln Ser His Pro Asn Met Val Ile Leu Gly  
 275 280 285  
 Glu Glu Val Ala Ala Ser Lys Leu Thr Ile Phe Asp Ile Thr Lys Gln  
 290 295 300  
 Ile Cys Asp Ala Val Gln Ala Arg Ala Glu Lys Asp Lys Asn His Gly  
 305 310 315  
 Val Ile Leu Ile Pro Glu Gly Leu Val Glu Ser Ile Pro Glu Leu Tyr  
 325 330 335  
 Ala Leu Leu Gln Glu Ile Asn Gly Leu His Gly Lys Gly Val Ser Ile  
 340 345 350  
 Glu Asn Ile Ser Ser Gln Leu Ser Pro Trp Ala Ser Ala Leu Phe Glu  
 355 360 365  
 Phe Leu Pro Gln Phe Ile Arg His Gln Leu Leu Leu Arg Pro Glu Ser  
 370 375 380  
 Asp Asp Ser Ala Gln Leu Ser Gln Ile Glu Thr Glu Lys Leu Leu Ala  
 385 390 395  
 Gln Leu Val Glu Thr Glu Met Asn Lys Arg Leu Lys Glu Gly Thr Tyr  
 405 410 415  
 Lys Gly Lys Lys Phe Asn Ala Ile Cys His Phe Phe Gly Tyr Gln Ala  
 420 425 430  
 Arg Gly Ala Met Pro Ser Lys Phe Asp Cys Asp Tyr Ala Tyr Val Leu  
 435 440 445  
 Gly His Val Ser Tyr His Ile Leu Ala Ala Gly Leu Asn Gly Tyr Met  
 450 455 460  
 Ala Thr Val Thr Asn Leu Lys Ser Pro Leu Asn Lys Trp Arg Cys Gly  
 465 470 475  
 Ala Ala Pro Ile Ser Ser Met Met Thr Val Lys Arg Trp Ser Arg Gly  
 485 490 495  
 Pro Ser Thr Thr Gln Ile Gly Lys Pro Ala Met His Met Ala Thr Val  
 500 505 510  
 Asp Leu Arg Gly Lys Ala Tyr Glu Leu Leu Arg Gln Asn Ser Ser Ser  
 515 520 525  
 Tyr Leu Leu Glu Asp Ile Tyr Arg Asn Pro Gly Pro Leu Gln Phe Glu  
 530 535 540  
 Gly Pro Gly Ala Asp Ser Lys Pro Ile Ser Leu Cys Val Glu Asp Gln  
 545 550 555  
 Asp Tyr Met Gly Arg Ile Lys Lys Leu Gln Glu Tyr Leu Glu Lys Val  
 565 570 575  
 Lys ser Ile Val Lys Pro Gly Cys Ser Gln Asp Val Leu Lys Ala Ala  
 580 585 590  
 Leu ser Ala Met Ser Ser Val Thr Glu Thr Leu Ala Ile Met Thr ser  
 595 600 605  
 ser ser Thr Gly Gln Ala Pro Leu  
 610 615

<210> 61  
 <211> 563  
 <212> PRT  
 <213> Lolium perenne

<400> 61  
Met Ala Ala Ala Ala Val Ala Thr Ser Asn Gly Ala Ser Ala Asn Gly  
1 5 10 15  
Pro Thr Pro Gly Arg Leu Ala Ser Val Tyr Ser Glu Val Gln Thr Ser  
20 25 30  
Arg Ile Ala His Ala Leu Pro Leu Pro Ser Val Leu Arg Ser His Phe  
35 40 45  
Thr Leu Ala Asp Gly Ala Ala Ser Ser Ala Thr Gly Asn Pro Glu Glu  
50 55 60  
Ile Ala Lys Leu Phe Pro Asn Leu Tyr Gly Gln Pro Ser Ala Ala Val  
65 70 75 80  
Val Pro Ser Ala Gln Pro Val Ala Thr Lys Pro Leu Lys Ile Gly Val  
85 90 95  
Val Leu Ser Gly Gly Gln Ala Pro Gly Gly His Asn Val Ile Cys Gly  
100 105 110  
Ile Phe Asp Tyr Leu Gln Glu Arg Ala Lys Gly Ser Thr Met Tyr Gly  
115 120 125  
Phe Lys Gly Gly Pro Ala Gly Val Met Lys Gly Lys Tyr Val Glu Leu  
130 135 140  
Asn Ala Asp Phe Val Tyr Pro Tyr Arg Asn Gln Gly Gly Phe Asp Met  
145 150 155 160  
Ile Cys Ser Gly Arg Asp Lys Ile Glu Thr Pro Glu Gln Phe Lys Gln  
165 170 175  
Ala Glu Asp Thr Val Thr Lys Leu Asp Leu Asp Gly Leu Val Val Ile  
180 185 190  
Gly Gly Asp Asp Ser Asn Thr Asn Ala Cys Leu Leu Gly Glu Tyr Phe  
195 200 205  
Arg Gly Arg Asn Leu Lys Thr Arg Val Ile Gly Cys Pro Lys Thr Ile  
210 215 220  
Asp Gly Asp Leu Lys Cys Lys Glu Val Pro Thr Ser Phe Gly Phe Asp  
225 230 235 240  
Thr Ala Cys Lys Ile Tyr Ser Glu Met Ile Gly Asn Val Met Thr Asp  
245 250 255  
Ala Arg Ser Thr Gly Lys Tyr Tyr His Phe Val Arg Leu Met Gly Arg  
260 265 270  
Ala Ala Ser His Ile Thr Leu Glu Cys Ala Leu Gln Thr His Pro Asn  
275 280 285  
Val Ser Leu Ile Gly Glu Glu Val Ala Glu Lys Lys Glu Thr Leu Lys  
290 295 300  
Gln Val Thr Asp Tyr Ile Thr Asp Val Ile Cys Lys Arg Ala Glu Leu  
305 310 315 320  
Gly Tyr Asn Tyr Gly Val Ile Leu Ile Pro Glu Gly Leu Ile Asp Phe  
325 330 335  
Ile Pro Glu Val Gln Lys Leu Ile Ala Glu Leu Asn Glu Ile Leu Ala  
340 345 350  
His Asp Val Val Asp Glu Ala Gly Ala Trp Lys Ser Lys Leu Gln Pro  
355 360 365  
Glu Ser Arg Gln Leu Phe Asp Phe Leu Pro Asn Thr Ile Gln Glu Gln  
370 375 380  
Leu Leu Leu Glu Arg Asp Pro His Gly Asn Val Gln Val Ala Lys Ile  
385 390 395 400  
Glu Thr Glu Lys Met Leu Ile Ala Met Val Glu Thr Glu Leu Glu Lys  
405 410 415 420  
Arg Arg Ser Ala Gly Lys Tyr Ser Ala His Phe Arg Gly Gln Ser His  
425 430 435 440  
Phe Phe Gly Tyr Glu Gly Arg Cys Gly Leu Pro Thr Asn Phe Asp Ser  
445 450 455 460  
Ser Tyr Cys Tyr Ala Leu Gly Tyr Gly Ala Gly Ala Leu Gln Phe  
465 470 475 480  
Gly Lys Thr Gly Leu Ile Ser Ser Val Gly Asn Leu Ala Ala Pro Val  
485 490 495 500  
Glu Glu Trp Thr Val Gly Gly Thr Pro Leu Thr Ala Leu Met Asp Val  
505 510 515 520  
Glu Arg Arg His Gly Lys Phe Lys Pro Val Ile Lys Lys Ala Met Val  
525 530 535 540  
Trp Ala Ile Lys Asn Arg Tyr Ile Ser Pro Gly Pro Ile Gln Phe Ser



530  
 Gly Pro Gly Ser Asp Ala Ser Asn His Thr Leu Met Leu Glu Leu Gly  
 545 550 555 560  
 Ala Gln Thr

<210> 62  
 <211> 563  
 <212> PRT  
 <213> Lolium perenne

<400> 62  
 Met Ala Ala Ala Ala Val Ala Thr Ser Asn Gly Ala Ser Ala Asn Gly  
 1 5 10 15  
 Pro Thr Pro Gly Arg Leu Ala Ser Val Tyr Ser Glu Val Gln Thr Ser  
 20 25 30  
 Arg Ile Ala His Ala Leu Pro Leu Pro Ser Val Leu Arg Ser His Phe  
 35 40 45  
 Thr Leu Ala Asp Gly Ala Ala Ser Ser Ala Thr Gly Asn Pro Glu Glu  
 50 55 60  
 Ile Ala Lys Leu Phe Pro Asn Leu Tyr Gly Gln Pro Ser Ala Ala Val  
 65 70 75 80  
 Val Pro Ser Ala Gln Pro Val Ala Thr Lys Pro Leu Lys Ile Gly Val  
 85 90 95  
 Val Leu Ser Gly Gln Ala Pro Gly His Asn Val Ile Cys Gly  
 100 105 110  
 Ile Phe Asp Tyr Leu Gln Glu Arg Ala Lys Gly Ser Thr Met Tyr Gly  
 115 120 125  
 Phe Lys Gly Gly Pro Ala Gly Val Met Lys Gly Lys Tyr Val Glu Leu  
 130 135 140  
 Asn Ala Asp Phe Val Tyr Pro Tyr Arg Asn Gln Gly Gly Phe Asp Met  
 145 150 155 160  
 Ile Cys Ser Gly Arg Asp Lys Ile Glu Thr Pro Glu Gln Phe Lys Gln  
 165 170 175  
 Ala Glu Asp Thr Val Thr Lys Leu Asp Leu Asp Gly Leu Val Val Ile  
 180 185 190  
 Gly Gly Asp Asp Ser Asn Thr Asn Ala Cys Leu Leu Gly Glu Tyr Phe  
 195 200 205  
 Arg Gly Arg Asn Leu Lys Thr Arg Val Ile Gly Cys Pro Lys Thr Ile  
 210 215 220  
 Asp Gly Asp Leu Lys Cys Lys Glu Val Pro Thr Ser Phe Gly Phe Asp  
 225 230 235 240  
 Thr Ala Cys Lys Ile Tyr Ser Glu Met Ile Gly Asn Val Met Thr Asp  
 245 250 255  
 Ala Arg Ser Thr Gly Lys Tyr Tyr His Phe Val Arg Leu Met Gly Arg  
 260 265 270  
 Ala Ala Ser His Ile Thr Leu Glu Cys Ala Leu Gln Thr His Pro Asn  
 275 280 285  
 Val Ser Leu Ile Gly Glu Glu Val Ala Glu Lys Lys Glu Thr Leu Lys  
 290 295 300  
 Gln Val Thr Asp Tyr Ile Thr Asp Val Ile Cys Lys Arg Ala Glu Leu  
 305 310 315 320  
 Gly Tyr Asn Tyr Gly Val Ile Leu Ile Pro Glu Gly Leu Ile Asp Phe  
 325 330 335  
 Ile Pro Glu Val Gln Lys Leu Ile Ala Glu Leu Asn Glu Ile Leu Ala  
 340 345 350  
 His Asp Val Val Asp Glu Ala Gly Ala Trp Lys Ser Lys Leu Gln Pro  
 355 360 365  
 Glu Ser Arg Gln Leu Phe Asp Phe Leu Pro Asn Thr Ile Gln Glu Gln  
 370 375 380  
 Leu Leu Leu Glu Arg Asp Pro His Gly Asn Val Gln Val Ala Lys Ile  
 385 390 395 400  
 Glu Thr Glu Lys Met Leu Ile Ala Met Val Glu Thr Glu Leu Glu Lys  
 405 410 415  
 Arg Arg Ser Ala Gly Lys Tyr Ser Ala His Phe Arg Gly Gln Ser His  
 420 425 430  
 Phe Phe Gly Tyr Glu Gly Arg Cys Gly Leu Pro Thr Asn Phe Asp Ser  
 435 440 445

Ser Tyr Cys Tyr Ala Leu Gly Tyr Gly Ala Gly Ala Leu Leu Gln Phe  
 450 455 460  
 Gly Lys Thr Gly Leu Ile Ser Ser Val Gly Asn Leu Ala Ala Pro Val  
 465 470 475 480  
 Glu Glu Trp Thr Val Gly Gly Thr Pro Leu Thr Ala Leu Met Asp Val  
 485 490 495  
 Glu Arg Arg His Gly Lys Phe Lys Pro Val Ile Lys Lys Ala Met Val  
 500 505 510  
 Glu Leu Asp Ala Ala Pro Phe Lys Lys Phe Ala Ser Met Arg Asp Glu  
 515 520 525  
 Trp Ala Ile Lys Asn Arg Tyr Ile Ser Pro Gly Pro Ile Gln Phe Ser  
 530 535 540  
 Gly Pro Gly Ser Asp Ala Ser Asn His Thr Leu Met Leu Glu Leu Gly  
 545 550 555 560  
 Ala Gln Thr

<210> 63  
 <211> 563  
 <212> PRT  
 <213> Festuca arundinacea

<400> 63  
 Met Ala Ala Ala Ala Val Ala Thr Ser Asn Gly Ala Ser Ala Asn Gly  
 1 5 10 15  
 Pro Thr Pro Gly Arg Leu Ala Ser Val Tyr Ser Glu Val Gln Thr Ser  
 20 25 30  
 Arg Ile Ala His Ala Leu Pro Leu Pro Ser Val Leu Arg Ser Asn Phe  
 35 40 45  
 Thr Leu Ala Asp Gly Pro Ala Ser Ser Ala Thr Gly Asn Pro Glu Glu  
 50 55 60  
 Ile Ala Lys Leu Phe Pro Asn Leu Tyr Gly Gln Pro Ser Ala Ala Val  
 65 70 75 80  
 Val Pro Ser Ala Glu Pro Val Pro Thr Lys Pro Leu Lys Ile Gly Val  
 85 90 95  
 Val Leu Ser Gly Gln Ala Pro Gly Gly His Asn Val Ile Cys Gly  
 100 105 110  
 Ile Phe Asp Tyr Leu Gln Glu Arg Ala Lys Gly Ser Thr Met Tyr Gly  
 115 120 125  
 Phe Lys Gly Gly Pro Ala Gly Ile Met Lys Gly Lys Tyr Ile Glu Leu  
 130 135 140  
 Asn Ala Asp Phe Val Tyr Pro Tyr Arg Asn Gln Gly Gly Phe Asp Met  
 145 150 155 160  
 Ile Cys Ser Gly Arg Asp Lys Ile Glu Thr Pro Glu Gln Phe Lys Gln  
 165 170 175  
 Ala Glu Asp Thr Val Asn Lys Leu Asp Leu Asp Gly Leu Val Val Ile  
 180 185 190  
 Gly Gly Asp Asp Ser Asn Thr Asn Ala Cys Leu Leu Gly Glu Tyr Phe  
 195 200 205  
 Arg Gly Arg Asn Leu Lys Thr Arg Val Ile Gly Cys Pro Lys Thr Ile  
 210 215 220  
 Asp Gly Asp Leu Lys Cys Lys Glu Val Pro Ile Ser Phe Gly Phe Asp  
 225 230 235 240  
 Thr Ala Cys Lys Ile Tyr Ser Glu Met Ile Gly Asn Val Met Thr Asp  
 245 250 255  
 Ala Arg Ser Thr Gly Lys Tyr Tyr His Phe Val Arg Leu Met Gly Arg  
 260 265 270  
 Ala Ala Ser His Ile Thr Leu Glu Cys Ala Leu Gln Thr His Pro Asn  
 275 280 285  
 Val Ser Leu Ile Gly Glu Glu Val Ala Glu Lys Lys Glu Thr Leu Lys  
 290 295 300  
 Gln Val Thr Asp Tyr Ile Thr Asp Val Ile Cys Lys Arg Ala Glu Leu  
 305 310 315 320  
 Gly Tyr Asn Tyr Gly Val Ile Leu Ile Pro Glu Gly Leu Ile Asp Phe  
 325 330 335  
 Ile Pro Glu Val Gln Lys Leu Ile Ala Glu Leu Asn Glu Ile Leu Ala  
 340 345 350  
 His Asp Val Val Asp Glu Ala Gly Ala Trp Lys Ser Lys Leu Gln Pro

355 360 365  
 Glu Ser Arg Gln Leu Phe Asp Phe Leu Pro Asn Thr Ile Gln Glu Gln  
 370 375 380  
 Leu Leu Leu Glu Arg Asp Pro His Gly Asn Val Gln Val Ala Lys Ile  
 385 390 395 400  
 Glu Thr Glu Lys Met Leu Ile Ala Met Val Glu Thr Glu Leu Glu Lys  
 405 410 415  
 Arg Arg Ala Ala Gly Lys Tyr Ser Ala His Phe Arg Gly Gln Ser His  
 420 425 430  
 Phe Phe Gly Tyr Glu Gly Arg Cys Gly Leu Pro Thr Asn Phe Asp Ser  
 435 440 445  
 Ser Tyr Cys Tyr Ala Leu Gly Tyr Gly Ala Gly Ala Leu Leu Gln Phe  
 450 455 460  
 Gly Lys Thr Gly Leu Ile Ser Ser Val Gly Asn Leu Ala Ala Pro Val  
 465 470 475 480  
 Glu Glu Trp Thr Val Gly Gly Thr Pro Leu Thr Ala Leu Met Asp Val  
 485 490 495  
 Glu Arg Arg His Gly Lys Phe Lys Pro Val Ile Lys Lys Ala Met Val  
 500 505 510  
 Glu Leu Asp Ala Ala Pro Phe Lys Lys Phe Ala Ser Met Arg Asp Glu  
 515 520 525  
 Trp Ala Ile Lys Asn Arg Tyr Ile Ser Pro Gly Pro Ile Gln Phe Ser  
 530 535 540  
 Gly Pro Gly Ser Asp Ala Ser Asn His Thr Leu Met Leu Glu Leu Gly  
 545 550 555 560  
 Ala Gln Ile

<210> 64  
 <211> 964  
 <212> PRT  
 <213> *Lotium perenne*

<400> 64  
 Met Val Gly Asn Asp Asn Trp Ile Asn Ser Tyr Leu Asp Ala Ile Leu  
 1 5 10 15  
 Asp Ala Gly Lys Ser Ser Ile Gly Gly Asp Arg Pro Ser Leu Leu Leu  
 20 25 30  
 Arg Glu Arg Gly His Phe Ser Pro Ala Arg Tyr Phe Val Glu Glu Val  
 35 40 45  
 Ile Thr Gly Tyr Asp Glu Thr Asp Leu Tyr Lys Thr Trp Leu Arg Ala  
 50 55 60  
 Asn Ala Met Arg Ser Pro Gln Glu Arg Asn Thr Arg Leu Glu Asn Met  
 65 70 75 80  
 Thr Trp Arg Ile Trp Asn Leu Ala Arg Lys Lys Lys Glu Leu Glu Lys  
 85 90 95  
 Glu Glu Ala Cys Arg Leu Leu Lys Arg His Pro Glu Thr Glu Lys Thr  
 100 105 110  
 Arg Thr Asp Ala Thr Ala Asp Met Ser Glu Asp Leu Phe Asp Gly Glu  
 115 120 125  
 Lys Gly Glu Asp Ala Gly Asp Pro Ser Val Ala Tyr Gly Asp Ser Thr  
 130 135 140  
 Thr Gly Ser Ser Pro Lys Thr Ser Ser Val Asp Lys Leu Tyr Ile Val  
 145 150 155 160  
 Leu Ile Ser Leu His Gly Leu Val Arg Gly Glu Asn Met Glu Leu Gly  
 165 170 175  
 Arg Asp Ser Asp Thr Gly Gly Gln Val Lys Tyr Val Val Glu Phe Ala  
 180 185 190  
 Lys Ala Leu Ser Ser Ser Pro Gly Val Tyr Arg Val Asp Leu Leu Thr  
 195 200 205  
 Arg Gln Ile Val Ala Pro Asn Phe Asp Arg Ser Tyr Gly Glu Pro Glu  
 210 215 220  
 Glu Met Leu Val Ser Thr Thr Phe Lys Asn Ser Lys His Glu Arg Gly  
 225 230 235 240  
 Val Asn Ser Gly Tyr Ile Ile Arg Ile Pro Phe Gly Pro Lys Asp  
 245 250 255  
 Lys Tyr Leu Ala Lys Glu His Met Trp Pro Phe Ile Gln Asp Phe Val  
 260 265 270

Asp Gly Ala Leu Ser His Ile Leu Arg Met Ser Lys Thr Ile Gly Glu  
 275 280  
 Glu Ile Gly Cys Gly His Pro Val Trp Pro Ala Val Ile His Gly His  
 290 300  
 Tyr Ala Ser Ala Gly Val Ala Ala Leu Leu Ser Gly Ala Leu Asn  
 305 310 315 320  
 Leu Pro Met Ala Phe Thr Gly His Phe Leu Gly Lys Asp Lys Leu Glu  
 325 330 335  
 Gly Leu Leu Lys Gln Gly Arg Gln Ser Arg Glu Gln Ile Asn Met Thr  
 340 345 350  
 Tyr Lys Ile Met Arg Arg Ile Glu Ala Glu Glu Leu Ser Leu Asp Ala  
 355 360 365  
 Ser Glu Ile Val Ile Ala Ser Thr Arg Gln Glu Ile Glu Glu Gln Trp  
 370 375 380  
 Asn Leu Tyr Asp Gly Phe Glu Val Ile Leu Ala Arg Lys Leu Arg Ala  
 385 390 395 400  
 Arg Val Lys Arg Gly Ala Asn Cys Tyr Gly Arg Tyr Met Pro Arg Met  
 405 410 415  
 Val Ile Ile Pro Gly Val Glu Phe Gly His Val Val His Asp Phe  
 420 425 430  
 Asp Met Asp Gly Glu Glu Glu Asn His Gly Pro Ala Ser Glu Asp Pro  
 435 440 445  
 Pro Ile Trp Ser Gln Ile Met Arg Phe Phe Thr Asn Pro Arg Lys Pro  
 450 455 460  
 Met Ile Leu Ala Val Ala Arg Pro Tyr Pro Glu Lys Asn Ile Thr Ser  
 465 470 475 480  
 Leu Val Lys Ala Phe Gly Glu Cys Arg Pro Leu Arg Glu Leu Ala Asn  
 485 490 495  
 Leu Thr Leu Ile Met Gly Asn Arg Glu Ala Ile Ser Lys Met His Asn  
 500 505 510  
 Thr Ser Ala Ser Val Leu Thr Ser Val Leu Thr Leu Ile Asp Glu Tyr  
 515 520 525  
 Asp Leu Tyr Gly Gln Val Ala Tyr Pro Lys His His Lys His Ser Glu  
 530 535 540  
 Val Pro Asp Ile Tyr Arg Leu Ala Thr Arg Thr Lys Gly Ala Phe Val  
 545 550 555 560  
 Asn Val Ala Tyr Phe Glu Gln Phe Gly Val Thr Leu Ile Glu Ala Ala  
 565 570 575  
 Met Asn Gly Leu Pro Val Ile Ala Thr Lys Asn Gly Ala Pro Val Glu  
 580 585 590  
 Ile Asn Gln Val Leu Asn Asn Gly Leu Leu Val Asp Pro His Asp Gln  
 595 600 605  
 Asn Ala Ile Ala Asp Ala Leu Tyr Lys Leu Leu Ser Glu Lys Gln Leu  
 610 615 620  
 Trp Ser Arg Cys Arg Glu Asn Gly Leu Lys Asn Ile His Gln Phe Ser  
 625 630 635 640  
 Trp Pro Glu His Cys Lys Asn His Leu Ser Arg Ile Leu Thr Leu Gly  
 645 650 655  
 Ala Arg Ser Pro Ala Ile Gly Ser Lys Glu Glu Arg Ser Asn Ala Pro  
 660 665 670  
 Ile Ser Gly Arg Lys His Ile Ile Val Ile Ser Val Asp Ser Val Asn  
 675 680 685  
 Lys Glu Asp Leu Val Arg Ile Ile Arg Asn Ala Ile Glu Ala Ala His  
 690 695 700  
 Thr Gln Asn Thr Pro Ala Ser Thr Gly Phe Val Leu Ser Thr Ser Leu  
 705 710 715 720  
 Thr Leu Ser Glu Ile Cys Ser Leu Leu Val Ser Val Gly Met His Pro  
 725 730 735  
 Ala Gly Phe Asp Ala Phe Ile Cys Asn Ser Gly Ser Ser Ile Tyr Tyr  
 740 745 750  
 Pro Ser Tyr Ser Gly Asn Thr Pro Ser Ser Ser Lys Val Thr His Val  
 755 760 765  
 Ile Asp Gln Asn His Gln Ser His Ile Glu Tyr Arg Trp Gly Gly Glu  
 770 775 780  
 Gly Leu Arg Lys Tyr Leu Val Lys Trp Ala Thr Ser Val Val Glu Arg  
 785 790 795 800  
 Lys Gly Arg Ile Glu Arg Gln Met Ile Phe Glu Asp Ser Glu His Ser  
 805 810 815

Ser Thr Tyr Cys Leu Ala Phe Lys Val Val Asn Pro Asn His Leu Pro  
 820 825 830  
 Pro Leu Lys Glu Leu Arg Lys Leu Met Arg Ile Gln Ser Leu Arg Cys  
 835 840 845  
 Asn Ala Leu Tyr Asn His Ser Ala Thr Arg Leu Ser Val Thr Pro Ile  
 850 855 860  
 His Ala Ser Arg Ser Gln Ala Ile Arg Tyr Leu Phe Ile Arg Trp Gly  
 865 870 875 880  
 Ile Glu Leu Pro Asn Ile Val Val Leu Val Gly Glu Ser Gly Asp Ser  
 885 890 895  
 Asp Tyr Glu Glu Leu Leu Gly Gly Leu His Arg Thr Ile Ile Leu Lys  
 900 905 910  
 Gly Asp Phe Asn Ile Ala Ala Asn Arg Ile His Thr Val Arg Arg Tyr  
 915 920 925  
 Pro Leu Gln Asp Val Val Ala Leu Asp Ser Ser Asn Ile Ile Glu Val  
 930 935 940  
 Glu Gly Cys Thr Thr Asp Val Ile Lys Ser Ala Leu Arg Gln Ile Gly  
 945 950 955 960  
 Val Pro Thr Gln

<210> 65  
 <211> 984  
 <212> PRT  
 <213> Festuca arundinacea

<220>  
 <221> VARIANT  
 <222> (1)...(984)  
 <223> Xaa = Any Amino Acid

<400> 65  
 Met Val Gly Gly Met Cys Gly Asn Asp Asn Trp Ile Asn Ser Tyr Leu  
 1 5 10 15  
 Asp Ala Ile Leu Asp Ala Gly Lys Gly Ala Pro Gly Gly Gly Ala Gly  
 20 25 30  
 Pro Gly Gly Gly Arg Gly Gly Gly Gly Ala Gly Asp Arg Pro  
 35 40 45  
 Ser Leu Leu Leu Arg Glu Arg Gly His Phe Ser Pro Ala Arg Tyr Phe  
 50 55 60  
 Val Glu Glu Val Ile Thr Gly Tyr Asp Glu Thr Asp Leu Tyr Lys Thr  
 65 70 75 80  
 Trp Ser Arg Ala Asn Ala Met Arg Ser Pro Gln Glu Arg Asn Thr Arg  
 85 90 95  
 Leu Glu Asn Met Thr Trp Arg Ile Trp Asn Leu Ala Arg Lys Lys Lys  
 100 105 110  
 Glu Xaa Glu Ala Glu Glu Ala Asn Arg Leu Leu Lys Arg Arg Leu Glu  
 115 120 125  
 Thr Glu Lys Pro Arg Thr Asp Ala Ala Ala Glu Met Ser Glu Asp Leu  
 130 135 140  
 Phe Glu Gly Gln Lys Gly Glu Asp Ala Gly Asp Ala Ser Val Ala Tyr  
 145 150 155 160  
 Gly Asp Ser Ser Ala Ser Asn Thr Pro Arg Ile Ser Ser Ile Asp Lys  
 165 170 175  
 Leu Tyr Ile Val Leu Ile Ser Leu His Gly Leu Val Arg Gly Glu Asn  
 180 185 190  
 Met Glu Leu Gly Arg Asp Ser Asp Thr Ser Gly Gln Val Lys Tyr Val  
 195 200 205  
 Val Glu Leu Ala Lys Ala Leu Ser Ser Cys Pro Gly Val Tyr Arg Val  
 210 215 220  
 Asp Leu Leu Thr Arg Gln Ile Leu Ala Pro Asn Tyr Asp Arg Gly Tyr  
 225 230 235 240  
 Gly Glu Pro Ser Glu Thr Leu Leu Pro Thr Asn Leu Lys Asn Phe Lys  
 245 250 255  
 His Glu Arg Gly Glu Asn Ser Gly Ala Tyr Ile Thr Arg Ile Pro Phe  
 260 265 270  
 Gly Pro Lys Asp Lys Tyr Leu Ala Lys Glu Gln Leu Trp Pro Tyr Val  
 275 280 285

Gln	Glu	Phe	Val	Asp	Gly	Ala	Leu	Ser	His	Ile	Val	Arg	Met	Ser	Lys
290	290					295					300				
Thr	Ile	Gly	Glu	Glu	Ile	Gly	Cys	Gly	His	Pro	Met	Trp	Pro	Ala	Ala
305	305				310					315					320
Ile	His	Gly	His	Tyr	Ala	Ser	Ala	Gly	Val	Ala	Ala	Ala	Leu	Leu	Ser
				325					330					335	
Gly	Ala	Leu	Asn	Val	His	Met	Ile	Phe	Thr	Gly	His	Phe	Leu	Gly	Arg
			340					345					350		
Asp	Lys	Leu	Glu	Gly	Leu	Leu	Lys	Gln	Gly	Lys	Gln	Thr	Arg	Glu	Glu
		355					360					365			
Ile	Asn	Met	Thr	Tyr	Lys	Ile	Met	Arg	Arg	Ile	Glu	Ala	Glu	Glu	Leu
	370					375					380				
Ser	Leu	Asp	Ala	Ser	Glu	Ile	Val	Ile	Ala	Ser	Thr	Arg	Gln	Glu	Ile
385					390					395					400
Glu	Glu	Gln	Trp	Asn	Leu	Tyr	Asp	Gly	Phe	Glu	Val	Met	Leu	Ala	Arg
				405					410					415	
Lys	Leu	Arg	Ala	Arg	Val	Lys	Arg	Gly	Ala	Asn	Cys	Tyr	Gly	Arg	Tyr
			420					425					430		
Met	Pro	Arg	Met	Val	Ile	Ile	Pro	Gly	Val	Glu	Phe	Gly	His	Met	
		435					440				445				
Ile	Gln	Asp	Phe	Asp	Met	Asp	Gly	Glu	Glu	Asp	Ser	Pro	Ser	Pro	Ala
	450					455					460				
Ser	Glu	Asp	Pro	Pro	Ile	Trp	Ser	Glu	Ile	Met	Arg	Phe	Phe	Thr	Asn
465					470					475					480
Pro	Arg	Lys	Pro	Leu	Ile	Leu	Ala	Val	Ala	Arg	Pro	Tyr	Pro	Glu	Lys
				485					490					495	
Asn	Ile	Thr	Thr	Leu	Val	Arg	Ala	Phe	Gly	Glu	Cys	Arg	Pro	Leu	Arg
			500					505					510		
Glu	Leu	Ala	Asn	Leu	Thr	Leu	Ile	Met	Gly	Asn	Arg	Glu	Ala	Ile	Ser
		515					520					525			
Lys	Met	Ser	Asn	Met	Ser	Ala	Ala	Val	Leu	Thr	Ser	Val	Leu	Thr	Leu
	530					535					540				
Ile	Asp	Glu	Tyr	Asp	Leu	Tyr	Gly	Gln	Val	Ala	Tyr	Pro	Lys	His	His
545					550					555					560
Lys	His	Ser	Glu	Val	Leu	Asp	Ile	Tyr	Arg	Leu	Ala	Ala	Arg	Thr	Lys
				565					570					575	
Gly	Ala	Phe	Val	Asn	Val	Ala	Tyr	Phe	Glu	Gln	Phe	Gly	Val	Thr	Leu
			580					585					590		
Ile	Glu	Ala	Ala	Met	His	Gly	Leu	Pro	Val	Ile	Ala	Thr	Lys	Asn	Gly
		595					600					605			
Ala	Pro	Val	Glu	Ile	His	Gln	Val	Leu	Asn	Asn	Gly	Leu	Leu	Val	Asp
	610					615					620				
Pro	His	Asp	Gln	Asn	Ala	Ile	Ala	Asp	Ala	Leu	Tyr	Lys	Leu	Leu	Ser
625					630					635					640
Glu	Lys	Gln	Leu	Trp	Ser	Arg	Cys	Arg	Glu	Asn	Gly	Leu	Lys	Asn	Ile
				645					650					655	
His	Gln	Phe	Ser	Trp	Pro	Glu	His	Cys	Lys	Asn	Tyr	Leu	Ser	Arg	Ile
			660					665					670		
Leu	Thr	Leu	Ser	Pro	Arg	Tyr	Pro	Ala	Phe	Ala	Ser	Asn	Asp	Asp	Gln
		675					680					685			
Ile	Lys	Ala	Pro	Ile	Lys	Gly	Arg	Lys	Tyr	Ile	Ile	Val	Ile	Ala	Val
	690					695					700				
Asp	Ser	Ala	Ser	Lys	Lys	Asp	Leu	Ala	Phe	Ile	Ile	Arg	Asn	Ser	Ile
705					710					715					720
Glu	Ala	Thr	Arg	Thr	Glu	Thr	Ser	Ser	Gly	Ser	Thr	Gly	Phe	Val	Leu
				725					730					735	
Ser	Thr	Ser	Leu	Thr	Ile	Ser	Glu	Ile	His	Ser	Leu	Leu	Ile	Ser	Ala
			740					745					750		
Gly	Met	Val	Pro	Thr	Asp	Phe	Asp	Ala	Phe	Ile	Cys	Asn	Ser	Gly	Ser
		755					760					765			
Asp	Leu	Phe	Tyr	Pro	Ser	Gln	Thr	Gly	Asp	Ser	Pro	Ser	Thr	Ser	Arg
	770					775					780				
Val	Thr	Phe	Ala	Leu	Asp	Arg	Asn	Tyr	Gln	Ser	Arg	Val	Glu	Tyr	His
785					790					795					800
Trp	Gly	Gly	Glu	Gly	Leu	Arg	Lys	Tyr	Leu	Val	Lys	Trp	Ala	Ser	Ser
				805					810					815	
Val	Val	Glu	Arg	Arg	Gly	Arg	Met	Glu	Lys	Gln	Val	Ile	Phe	Asp	Asp
			820					825					830		

Ser Glu His Ser Ser Thr Cys Cys Leu Ala Phe Arg Val Val Asn Pro  
 835 840 845  
 Asn Tyr Leu Pro Pro Leu Lys Glu Leu Gln Lys Leu Met Arg Val Gln  
 850 855 860  
 Ser Leu Arg Cys His Ala Leu Tyr Asn His Ser Ala Thr Arg Leu Ser  
 865 870 875 880  
 Val Ile Pro Ile His Ala Ser Arg Ser Gln Ala Ile Arg Tyr Leu Ser  
 885 890 895  
 Val Arg Trp Gly Ile Glu Leu Pro Asn Val Val Ile Leu Val Gly Glu  
 900 905 910  
 Ser Gly Asp Ser Asp Tyr Glu Glu Phe Gly Gly Leu His Lys Thr  
 915 920 925  
 Val Val Leu Asn Gly Glu Phe Asn Thr Pro Ala Asn Arg Ile His Thr  
 930 935 940  
 Val Arg Arg Tyr Pro Leu Gln Asp Val Ile Ala Leu Asp Cys Ser Asn  
 945 950 955 960  
 Ile Val Gly Val Gln Gly Cys Ser Thr Asp Cys Met Arg Ser Thr Leu  
 965 970 975  
 Glu Lys Leu Gly Ile Pro Thr Lys  
 980

<210> 66  
 <211> 522  
 <212> PRT  
 <213> Festuca arundinacea

<400> 66  
 Met Val Arg Gly Gly Gly Asn Gly Glu Val Glu Leu Ser Val Gly Ala  
 1 5 10 15  
 Gly Gly Gly Gly Gly Ala Gly Gly Leu Val Glu Pro Pro Val Pro  
 20 25 30  
 Ile Ser Leu Gly Arg Leu Val Leu Ala Gly Met Val Ala Gly Gly Val  
 35 40 45  
 Gln Tyr Gly Trp Ala Leu Gln Leu Ser Leu Leu Thr Pro Tyr Val Gln  
 50 55 60  
 Thr Leu Gly Leu Ser His Ala Leu Thr Ser Phe Met Trp Leu Cys Gly  
 65 70 75 80  
 Pro Ile Ala Gly Leu Val Val Gln Pro Cys Val Gly Leu Tyr Ser Asp  
 85 90 95  
 Lys Cys Thr Ser Arg Trp Gly Arg Arg Pro Phe Ile Met Thr Gly  
 100 105 110  
 Cys Val Leu Ile Cys Ile Ala Val Val Ile Val Gly Phe Ser Ala Asp  
 115 120 125  
 Ile Gly Ala Ala Leu Gly Asp Ser Lys Glu Glu Cys Ser Leu Tyr His  
 130 135 140  
 Gly Pro Arg Trp His Ala Ala Ile Val Tyr Val Leu Gly Phe Trp Leu  
 145 150 155 160  
 Leu Asp Phe Ser Asn Asn Thr Val Gln Gly Pro Ala Arg Ala Leu Met  
 165 170 175  
 Ala Asp Leu Ser Gly Lys Tyr Gly Pro Ser Ala Ala Asn Ser Ile Phe  
 180 185 190  
 Cys Ser Trp Met Ala Leu Gly Asn Ile Leu Gly Tyr Ser Ser Gly Ser  
 195 200 205  
 Thr Asp Lys Trp His Lys Trp Phe Pro Phe Leu Arg Thr Arg Ala Cys  
 210 215 220  
 Cys Glu Ala Cys Ala Asn Leu Lys Gly Ala Phe Leu Val Ala Val Leu  
 225 230 235 240  
 Phe Leu Cys Met Cys Leu Val Ile Thr Leu Ile Phe Ala Lys Glu Val  
 245 250 255  
 Pro Tyr Lys Arg Ile Ala Pro Leu Pro Thr Lys Ala Asn Gly Gln Val  
 260 265 270  
 Glu Val Glu Pro Ser Gly Pro Leu Ala Val Phe Gln Gly Ile Arg Asn  
 275 280 285  
 Leu Pro Ser Gly Met Pro Ser Val Leu Leu Val Thr Gly Leu Thr Trp  
 290 295 300  
 Leu Ser Trp Phe Pro Phe Ile Leu Tyr Asp Thr Asp Trp Met Gly Arg  
 305 310 315 320  
 Glu Ile Tyr His Gly Asp Pro Lys Gly Thr Pro Ala Glu Met Ser Ala

Phe Gln Asp Gly Val Arg Ala Gly Ala Phe Gly Leu Leu Leu Asn Ser  
 Ile Ile Leu Gly Phe Ser Ser Phe Leu Ile Glu Pro Met Cys Lys Arg  
 Leu Gly Pro Arg Val Val Trp Val Ser Ser Asn Phe Leu Val Cys Ile  
 Ala Met Ala Ala Thr Ala Ile Ile Ser Trp Trp Ser Thr Lys Glu Phe  
 His Glu Tyr Val Gln His Ala Ile Thr Ala Ser Lys Asp Ile Lys Ile  
 Val Cys Met Ala Leu Phe Ala Phe Leu Gly Val Pro Leu Ala Ile Leu  
 Tyr Ser Val Pro Phe Ala Val Thr Ala Gln Leu Ala Ala Ser Lys Gly  
 Gly Gly Gln Gly Leu Cys Thr Gly Val Leu Asn Ile Ser Ile Val Ile  
 Pro Gln Val Ile Ile Ala Leu Gly Ala Gly Pro Trp Asp Gln Leu Phe  
 Gly Lys Gly Asn Ile Pro Ala Phe Ala Ala Ser Ala Phe Ala Leu  
 Ile Gly Gly Ile Val Gly Ile Phe Leu Leu Pro Lys Ile Ser Arg Arg  
 Ser Phe Arg Ala Val Ser Thr Gly Gly His  
 325 330 335  
 340 345 350  
 355 360 365  
 370 375 380  
 385 390 395  
 400 405 410 415  
 420 425 430 435 440 445  
 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520

&lt;210&gt; 67

&lt;211&gt; 407

&lt;212&gt; PRT

&lt;213&gt; Festuca arundinacea

&lt;400&gt; 67

Ile Cys Val Ala Val Val Val Val Gly Phe Ser Ala Asp Ile Gly Ala  
 1 5 10 15  
 Ala Leu Gly Asp Ser Lys Glu Glu Cys Ser Leu Tyr His Gly Pro Arg  
 20 25 30  
 Trp His Ala Ile Val Tyr Val Leu Gly Phe Trp Leu Leu Asp Phe  
 35 40 45  
 Ser Asn Asn Thr Val Gln Gly Pro Ala Arg Ala Leu Met Ala Asp Leu  
 50 55 60  
 Ser Gly Lys Tyr Gly Pro Ser Ala Ala Asn Ser Ile Phe Cys Ser Trp  
 65 70 75 80  
 Met Ala Leu Gly Asn Ile Leu Gly Tyr Ser Ser Gly Ser Thr Asp Lys  
 85 90 95  
 Trp His Lys Trp Phe Pro Phe Leu Arg Thr Arg Ala Cys Cys Glu Ala  
 100 105 110 115  
 Cys Ala Asn Leu Lys Gly Ala Phe Leu Val Ala Val Leu Phe Leu Cys  
 120 125  
 Phe Cys Leu Val Ile Thr Leu Ile Phe Ala Lys Glu Val Pro Tyr Lys  
 130 135 140  
 Arg Ile Ala Pro Leu Pro Thr Lys Ala Asn Gly Gln Val Glu Val Glu  
 145 150 155 160  
 Pro Ser Gly Pro Leu Ala Val Phe Gln Gly Phe Arg Asn Leu Pro Ser  
 165 170 175  
 Gly Met Pro Ser Val Leu Leu Val Thr Gly Leu Thr Trp Leu Ser Trp  
 180 185 190  
 Phe Pro Phe Ile Leu Tyr Asp Thr Asp Trp Met Gly Arg Glu Ile Tyr  
 195 200 205  
 His Gly Asp Pro Lys Gly Thr Pro Ala Glu Ala Ser Ala Phe Gln Asp  
 210 215 220  
 Gly Val Arg Ala Gly Ala Phe Gly Leu Leu Leu Asn Ser Ile Ile Leu  
 225 230 235 240  
 Gly Phe Ser Ser Phe Leu Ile Glu Pro Met Cys Lys Arg Leu Gly Pro  
 245 250 255  
 Arg Val Val Trp Val Ser Ser Asn Leu Leu Val Cys Ile Ala Met Ala  
 260 265 270  
 Ala Thr Ala Ile Ile Ser Trp Trp Ser Thr Lys Glu Phe His Glu Tyr  
 275 280 285



Val Gln His Ala Ile Thr Ala Ser Lys Asp Ile Lys Ile Val Cys Met  
 290 295 300  
 Val Leu Phe Ala Phe Leu Gly Val Pro Leu Ala Ile Leu Tyr Ser Val  
 305 310 315 320  
 Pro Phe Ala Val Thr Ala Gln Leu Ala Ala Asn Lys Gly Gly Gly Gln  
 325 330 335  
 Gly Leu Cys Thr Gly Val Leu Asn Ile Ser Ile Val Ile Pro Gln Val  
 340 345 350  
 Ile Ile Ala Leu Gly Ala Gly Pro Trp Asp Gln Leu Phe Gly Lys Gly  
 355 360 365  
 Asn Ile Pro Ala Phe Ala Ala Ser Ala Phe Ala Leu Ile Gly Gly  
 370 375 380  
 Ile Val Gly Ile Phe Leu Leu Pro Lys Ile Ser Arg His Ser Phe Arg  
 385 390 395 400  
 Ala Val Ser Thr Gly Gly His  
 405

<210> 68  
 <211> 522  
 <212> PRT  
 <213> Festuca arundinacea

<400> 68  
 Met Val Arg Gly Gly Gly Asn Ser Glu Val Glu Leu Ser Val Gly Ala  
 1 5 10 15  
 Gly Gly Gly Gly Gly Ala Gly Gly Leu Val Glu Pro Pro Val Pro  
 20 25 30  
 Ile Ser Leu Gly Arg Leu Val Phe Ala Gly Met Val Ala Gly Gly Val  
 35 40 45  
 Gln Tyr Gly Trp Ala Leu Gln Leu Ser Leu Leu Thr Pro Tyr Val Gln  
 50 55 60  
 Thr Leu Gly Leu Ser His Ala Leu Thr Ser Phe Met Trp Leu Cys Gly  
 65 70 75 80  
 Pro Ile Ala Gly Leu Val Val Gln Pro Cys Val Gly Leu Tyr Ser Asp  
 85 90 95  
 Lys Cys Thr Ser Arg Trp Gly Arg Arg Pro Phe Ile Met Thr Gly  
 100 105 110  
 Cys Val Leu Ile Cys Ile Ala Val Val Ile Val Gly Phe Ser Ala Asp  
 115 120 125  
 Ile Gly Ala Ala Leu Gly Asp Ser Lys Glu Glu Cys Ser Leu Tyr His  
 130 135 140  
 Gly Pro Arg Trp His Ala Ala Ile Val Tyr Val Leu Gly Phe Trp Leu  
 145 150 155 160  
 Leu Asp Phe Ser Asn Thr Val Gln Gly Pro Ala Arg Ala Leu Met  
 165 170 175  
 Ala Asp Leu Ser Gly Lys Tyr Gly Pro Ser Ala Ala Asn Ser Ile Phe  
 180 185 190  
 Cys Ser Trp Met Ala Leu Gly Asn Ile Leu Gly Tyr Ser Ser Gly Ser  
 195 200 205  
 Thr Asp Lys Trp His Lys Trp Phe Pro Phe Leu Arg Thr Arg Ala Cys  
 210 215 220  
 Cys Glu Ala Cys Ala Asn Leu Lys Gly Ala Phe Leu Val Ala Val Leu  
 225 230 235 240  
 Phe Leu Cys Phe Cys Leu Val Ile Thr Leu Ile Phe Ala Lys Glu Val  
 245 250 255  
 Pro Tyr Lys Arg Ile Ala Pro Leu Pro Thr Lys Ala Asn Gly Gln Val  
 260 265 270  
 Glu Val Glu Pro Ser Gly Pro Leu Ala Val Phe Gln Gly Phe Arg Asn  
 275 280 285  
 Leu Pro Ser Gly Met Pro Ser Val Leu Leu Val Thr Gly Leu Thr Trp  
 290 295 300  
 Leu Ser Trp Phe Pro Phe Ile Leu Tyr Asp Thr Asp Trp Met Gly Arg  
 305 310 315 320  
 Glu Ile Tyr His Gly Asp Pro Lys Gly Thr Pro Ala Glu Ala Ser Ala  
 325 330 335  
 Phe Gln Asp Gly Val Arg Ala Gly Ala Phe Gly Leu Leu Leu Asn Ser  
 340 345 350  
 Ile Ile Leu Gly Phe Ser Ser Phe Leu Ile Glu Pro Met Cys Lys Arg  
 Page 54

Leu Gly 355 Pro Arg Val Val Trp 360 Val Ser Ser Asn Leu 365 Leu Val Cys Ile  
 Ala 370 Met Ala Ala Thr Ala 375 Ile Ile Ser Trp Trp 380 Ser Thr Lys Glu Phe  
 385 His Glu Tyr Val Gln 390 His Ala Ile Thr Ala 395 Ser Lys Asp Ile Lys 400 Ile  
 Val Cys Met Val 405 Leu Phe Ala Phe Leu 410 Gly Val Pro Leu Ala 415 Ile Leu  
 Tyr Ser Val 420 Pro Phe Ala Val Thr 425 Ala Gln Leu Ala 430 Asn Lys Gly  
 Gly Gly Gln Gly Leu Cys Thr Gly Val Leu Asn Ile Ser Ile Val Ile  
 435 440 445  
 Pro Gln Val Ile Ile Ala Leu Gly Ala Gly Pro Trp Asp Gln Leu Phe  
 450 455 460 465  
 Gly Lys Gly Asn Ile Pro Ala Phe Ala Ala Ser Ala Phe Ala Leu  
 470 475 480  
 Ile Gly Gly Ile Val Gly Ile Phe Leu 490 Pro Lys Ile Ser Arg His  
 485 495 500 505 510  
 Ser Phe Arg Ala Val Ser Thr Gly Gly His  
 515 520

<210> 69  
 <211> 506  
 <212> PRT  
 <213> Lolium perenne

<400> 69  
 Met Pro Pro Pro Arg Arg Pro Thr Thr Gly Gly Thr Thr Thr Thr Ser  
 1 5 10 15  
 Ala Ala Leu Pro Pro Pro Arg Lys Val Pro Leu Arg Ser Leu Leu Arg  
 20 25 30  
 Ala Ala Ser Val Ala Cys Gly Val Gln Phe Gly Trp Ala Leu Gln Leu  
 35 40 45  
 Ser Leu Leu Thr Pro Tyr Val Gln Glu Leu Gly Ile Pro His Ala Phe  
 50 55 60  
 Ala Ser Leu Val Trp Leu Cys Gly Pro Leu Ser Gly Leu Leu Val Gln  
 65 70 75 80  
 Pro Leu Ile Gly His Leu Ser Asp Arg Ile Ala Pro Ala Asp Ser Pro  
 85 90 95  
 Leu Gly Arg Arg Arg Pro Phe Ile Ala Ala Gly Ala Ala Ser Ile Ala  
 100 105 110  
 Phe Ser Val Leu Thr Val Gly Phe Ser Ala Asp Leu Gly Arg Leu Phe  
 115 120 125  
 Gly Asp Asn Val Arg Pro Gly Ser Thr Arg Tyr Gly Ala Ile Ile Val  
 130 135 140  
 Tyr Met Ile Gly Phe Trp Leu Leu Asp Val Gly Asn Asn Ala Thr Gln  
 145 150 155 160  
 Gly Pro Cys Arg Ala Phe Leu Ala Asp Leu Thr Glu Asn Asp Pro Arg  
 165 170 175  
 Arg Thr Arg Ile Ala Asn Ala Tyr Phe Ser Leu Phe Met Ala Leu Gly  
 180 185 190  
 Asn Ile Leu Gly Tyr Ala Thr Gly Ala Tyr Ser Gly Trp Tyr Lys Ile  
 195 200 205  
 Phe pro Phe Thr Ile Thr Glu Ser Cys Gly Val Ser Cys Ala Asn Leu  
 210 215 220  
 Lys Ser Ala Phe Leu Leu Asp Ile Ile Ile Leu Ala Ile Thr Thr Tyr  
 225 230 235 240  
 Val Thr Val Val Thr Val Gln Asp Asn Pro Thr Phe Gly Ser Asp Glu  
 245 250 255  
 Ala Ala Pro Arg Pro Ser Ser His Glu Glu Ala Phe Leu Phe Glu  
 260 265 270  
 Leu Phe Gly Ser Phe Lys Tyr Phe Thr Met Pro Val Trp Met Val Leu  
 275 280 285  
 Ile Val Thr Ser Leu Thr Trp Ile Gly Trp Phe Pro Phe Ile Leu Phe  
 290 295 300  
 Asp Thr Asp Trp Met Gly Arg Glu Ile Tyr Arg Gly Ser Pro Glu Ile  
 305 310 315 320

Val Ala Asp Thr Gln Lys Tyr His Asp Gly Val Arg Met Gly Ser Phe  
 325 330 335  
 Gly Leu Met Leu Asn Ser Val Leu Leu Gly Ile Thr Ser Val Val Thr  
 340 345 350  
 Glu Lys Leu Cys Arg Lys Trp Gly Ala Gly Leu Val Trp Gly Val Ser  
 355 360 365  
 Asn Ile Ile Met Ala Leu Cys Phe Val Ala Met Leu Val Ile Thr Tyr  
 370 375 380  
 Val Ala Gln Asn Leu Asp Tyr Gly Pro Ser Gly Ala Pro Pro Thr Gly  
 385 390 395 400  
 Ile Val Val Ala Ser Leu Thr Val Phe Thr Ile Leu Gly Ala Pro Leu  
 405 410 415  
 Ser Ile Thr Tyr Ser Ile Pro Tyr Ala Met Ala Thr Ser Arg Val Glu  
 420 425 430  
 Asn Leu Gly Leu Gly Gln Gly Leu Ala Met Gly Ile Leu Asn Leu Ser  
 435 440 445  
 Ile Val Ile Pro Gln Ile Ile Val Ser Leu Gly Ser Gly Pro Trp Asp  
 450 455 460  
 Ser Leu Phe Gly Gly Gly Asn Ala Pro Ser Phe Trp Val Ala Ala Ala  
 465 470 475 480  
 Ala Ser Phe Ile Gly Gly Leu Val Ala Ile Leu Gly Leu Pro Arg Ala  
 485 490 495  
 Arg Ile Ala Pro Lys Lys Arg Ser Gln Arg  
 500 505

<210> 70  
 <211> 504  
 <212> PRT  
 <213> Festuca arundinacea

<400> 70  
 Met Pro Pro Pro Arg Arg Pro Asn Ala Gly Gly Thr Thr Ser Ala Pro  
 1 5 10 15  
 Leu Pro Pro Pro Arg Lys Val Pro Leu Arg Ser Leu Leu Arg Ala Ala  
 20 25 30  
 Ser Val Ala Cys Gly Val Gln Phe Gly Trp Ala Leu Gln Leu Ser Leu  
 35 40 45  
 Leu Thr Pro Tyr Val Gln Glu Leu Gly Ile Pro His Ala Phe Ala Ser  
 50 55 60  
 Leu Val Trp Leu Cys Gly Pro Leu Ser Gly Leu Val Gln Pro Leu  
 65 70 75 80  
 Ile Gly His Leu Ser Asp Arg Ile Ala Pro Ala Asp Ser Pro Leu Gly  
 85 90 95  
 Arg Arg Arg Pro Phe Ile Ala Ala Gly Ala Ala Ser Ile Ala Phe Ser  
 100 105 110  
 Val Leu Thr Val Gly Phe Ser Ala Asp Leu Gly Arg Leu Phe Gly Asp  
 115 120 125  
 Asn Ile Arg Pro Gly Ser Thr Arg Phe Gly Ala Ile Ile Val Tyr Met  
 130 135 140  
 Ile Gly Phe Trp Leu Leu Asp Val Gly Asn Asn Ala Thr Gln Gly Pro  
 145 150 155 160  
 Cys Arg Ala Phe Leu Ala Asp Leu Thr Glu Asn Asp Pro Arg Arg Thr  
 165 170 175  
 Arg Ile Ala Asn Ala Tyr Phe Ser Leu Phe Met Ala Leu Gly Asn Ile  
 180 185 190  
 Leu Gly Tyr Ala Thr Gly Ala Tyr Ser Gly Trp Tyr Lys Ile Phe Pro  
 195 200 205  
 Phe Thr Ile Thr Glu Ser Cys Gly Val Ser Cys Ala Asn Leu Lys Ser  
 210 215 220  
 Ala Phe Leu Leu Asp Ile Ile Ile Leu Ala Ile Thr Thr Tyr Val Thr  
 225 230 235 240  
 Val Val Thr Val Gln Asp Asn Pro Thr Phe Gly Ser Asp Glu Ala Ala  
 245 250 255  
 Pro Arg Pro Ser Ser His Glu Glu Glu Ala Phe Leu Phe Glu Leu Phe  
 260 265 270  
 Gly Ser Phe Lys Tyr Phe Thr Leu Pro Val Trp Met Val Leu Ile Val  
 275 280 285  
 Thr Ser Leu Thr Trp Ile Gly Trp Phe Pro Phe Ile Leu Phe Asp Thr

290 295 300  
 Asp Trp Met Gly Arg Glu Ile Tyr Arg Gly Ser Pro Glu Ile Val Ala  
 305 310 315 320  
 Asp Thr Gln Lys Tyr His Asp Gly Val Arg Met Gly Ser Phe Gly Leu  
 325 330 335  
 Met Leu Asn Ser Val Leu Leu Gly Ile Thr Ser Val Val Met Glu Lys  
 340 345 350  
 Leu Cys Arg Lys Trp Gly Ala Gly Leu Val Trp Gly Val Ser Asn Ile  
 355 360 365  
 Ile Met Ala Leu Cys Phe Val Ala Met Leu Ile Ile Thr Tyr Val Ala  
 370 375 380  
 Lys Asn Leu Asp Tyr Gly Pro Ser Gly Ala Pro Thr Gly Ile Val  
 385 390 395 400  
 Val Ala Ser Leu Ala Val Phe Thr Ile Leu Gly Ala Pro Leu Ser Ile  
 405 410 415  
 Thr Tyr Ser Ile Pro Tyr Ala Met Ala Thr Ser Arg Val Glu Asn Leu  
 420 425 430  
 Gly Leu Gly Gln Gly Leu Ala Met Gly Ile Leu Asn Leu Ser Ile Val  
 435 440 445  
 Ile Pro Gln Ile Ile Val Ser Leu Gly Ser Gly Pro Trp Asp Ser Leu  
 450 455 460  
 Phe Gly Gly Gly Asn Ala Pro Ser Phe Trp Val Ala Ala Ala Ala Ser  
 465 470 475 480  
 Phe Ile Gly Gly Leu Val Ala Ile Leu Gly Leu Pro Arg Ala Arg Ile  
 485 490 495  
 Ala Pro Lys Lys Arg Ser Gln Arg  
 500

<210> 71  
 <211> 508  
 <212> PRT  
 <213> Lolium perenne

<400> 71  
 Met Val Asp Gln Asp His Asp Gly Arg Arg Arg Gln Glu Glu Ala Thr  
 1 5 10 15  
 Ala Val Ala Ala Ser Ser Val Pro Leu Leu Glu Lys Lys Pro Gly Asp  
 20 25 30  
 Val Pro Tyr Tyr Val Glu Gly Cys Pro Gly Cys Ala Val Asp Arg Arg  
 35 40 45  
 Lys Ala Thr Asp Pro Gly Ile Pro Tyr Gly Ser Phe Ile Tyr Ile Trp  
 50 55 60  
 Val Val Ile Leu Cys Thr Ala Ile Pro Ile Ser Leu Phe Pro Phe  
 65 70 75 80  
 Leu Tyr Phe Met Ile Arg Asp Leu His Ile Ala Glu Arg Thr Glu Asp  
 85 90 95  
 Ile Gly Phe Tyr Ala Gly Phe Val Gly Ala Ala Phe Met Phe Gly Arg  
 100 105 110  
 Cys Leu Thr Ser Thr Ile Trp Gly Ile Ala Ala Asp Arg Ile Gly Arg  
 115 120 125  
 Lys Pro Val Val Ile Phe Gly Val Phe Ser Val Val Ile Phe Asn Ala  
 130 135 140  
 Leu Phe Gly Leu Ser Val Thr Tyr Trp Met Ala Ile Ala Thr Arg Phe  
 145 150 155 160  
 Leu Leu Gly Ala Leu Asn Gly Leu Leu Gly Pro Met Lys Ala Tyr Ala  
 165 170 175  
 Ile Glu Val Cys Arg Pro Glu His Glu Ala Leu Ala Leu Ser Leu Val  
 180 185 190  
 Ser Thr Ala Trp Gly Ile Gly Leu Ile Ile Gly Pro Ala Leu Gly Gly  
 195 200 205  
 Tyr Leu Ala Leu Pro Ala Glu Lys Tyr Pro Asn Ile Phe Ser Pro Asp  
 210 215 220  
 Ser Leu Phe Gly Arg Phe Pro Tyr Phe Leu Pro Cys Leu Cys Thr Ser  
 225 230 235 240  
 Val Phe Ala Ala Ala Val Leu Ile Gly Cys Ile Trp Met Pro Glu Thr  
 245 250 255  
 Leu His Lys His Lys Val Asn Glu Asn Arg Asn Gln Ser Val Glu Ser  
 260 265 270

Leu Glu Ala His Leu Ile Asp Pro Lys Glu Lys Val Glu Gln Ser Asn  
 275 280 285  
 Ser Pro Asp Thr Lys Lys Ser Leu Phe Lys Asn Trp Pro Leu Met Ser  
 290 300  
 Ser Ile Ile Val Tyr Cys Val Phe Ser Phe His Asp Met Ala Tyr Thr  
 305 310 315 320  
 Glu Val Phe Ser Leu Trp Ala Glu Ser Asp Arg Thr Tyr Gly Gly Leu  
 325 330 335  
 Ser Leu Ser Ser Glu Asp Val Gly Gln Thr Leu Ala Ile Thr Gly Ser  
 340 345 350  
 Ser Leu Leu Val Tyr Gln Leu Phe Leu Tyr Pro Arg Ile Asn Arg Val  
 355 360 365  
 Leu Gly Pro Ile Lys Ser Ser Gln Ile Ala Ala Gly Ile Cys Ile Pro  
 370 375 380  
 Ile Leu Phe Ala Tyr Pro Tyr Met Thr Tyr Leu Ser Glu Pro Gly Leu  
 385 390 395 400  
 Ser Ile Val Leu Asn Ile Ala Ser Val Ile Lys Asn Asn Leu Gly Val  
 405 410 415  
 Thr Ile Ile Thr Gly Thr Phe Ile Leu Gln Asn Asn Ala Val Pro Gln  
 420 425 430  
 Asp Gln Arg Gly Ala Ala Asn Gly Leu Ala Met Thr Gly Met Ser Phe  
 435 440 445  
 Phe Lys Ala Val Ala Pro Ala Gly Ala Gly Ile Val Phe Ser Trp Ala  
 450 455 460  
 Gln Lys Arg Gln His Ala Phe Phe Phe Pro Gly Asp Gln Met Val Phe  
 465 470 475 480  
 Phe Leu Leu Asn Ile Ile Glu Leu Leu Gly Leu Leu Leu Thr Phe Lys  
 485 490 495  
 Phe Phe Leu Ala Val Pro Asp Lys Ser Asp Ser Asn  
 500 505

<210> 72  
 <211> 522  
 <212> PRT  
 <213> Lolium perenne

<400> 72  
 Met Ser Ser Met Gln Phe Ser Ser Val Leu Pro Leu Glu Gly Lys Ala  
 1 5 10 15  
 Cys Val Cys Pro Val Arg Ser Ala Asn Gln Cys Glu Arg Leu Lys  
 20 25 30  
 Val Gly Asp Ser Ser Ser Leu Arg His Glu Met Ala Leu Arg Arg Lys  
 35 40 45  
 Cys Asn Gly Ala Arg Gly Gly Gly Ala Ala Asn Gly Ala Gln Cys Val  
 50 55 60  
 Leu Thr Ser Asp Ala Ser Pro Asp Thr Leu Val Val Arg Ser Ser Phe  
 65 70 75 80  
 Arg Arg Asn Tyr Ala Asp Pro Asn Glu Val Ala Ala Val Ile Leu Gly  
 85 90 95  
 Gly Gly Thr Gly Thr Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr  
 100 105 110  
 Pro Ala Val Pro Ile Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met  
 115 120 125  
 Ser Asn Cys Phe Asn Ser Gly Ile Asn Lys Ile Phe Val Met Thr Gln  
 130 135 140  
 Phe Asn Ser Ala Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Gly  
 145 150 155 160  
 Gly Gly Ile Asn Phe Thr Asp Gly Ser Val Glu Val Leu Ala Ala Thr  
 165 170 175  
 Gln Met Pro Gly Glu Ala Ala Gly Trp Phe Arg Gly Thr Ala Asp Ala  
 180 185 190  
 Val Arg Lys Phe Ile Trp Val Leu Glu Asp Tyr Tyr Lys His Lys Ser  
 195 200 205  
 Ile Glu His Ile Leu Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asp  
 210 215 220  
 Tyr Met Glu Leu Val Gln Lys His Val Asp Asp Asn Ala Asp Ile Thr  
 225 230 235 240  
 Leu Ser Cys Ala Pro Val Gly Glu Ser Arg Ala Ser Glu Tyr Gly Leu

Val Lys Phe Asp Ser Ser Gly Arg Val Ile Gln Phe Ser Glu Lys Pro  
 Lys Gly Ala 260 Leu Glu Ala Met Lys Val Asp Thr Ser Phe Leu Asn  
 Phe Ala Ile Asp Asp Pro Ala Lys Asn Pro Tyr Ile Ala Ser Met Gly  
 Val Tyr Val Phe Lys Arg Glu Val Leu Leu Asn Leu Lys Ser Arg  
 Tyr Thr Glu Leu His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Leu  
 His Asp His Asn Val Gln Ala Tyr Val Phe Thr Asp Tyr Trp Glu Asp  
 Ile Gly Thr Ile Arg Ser Phe Phe Asp Ala Asn Met Ala Leu Cys Glu  
 Gln Pro Pro Lys Phe Glu Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr  
 Ser Pro Arg Tyr Leu Pro Pro Thr Lys Ser Asp Lys Cys Arg Ile Lys  
 Glu Ala Ile Ile Ser His Gly Cys Phe Leu Arg Glu Cys Thr Ile Glu  
 His Ser Ile Ile Gly Val Arg Ser Arg Leu Asn Ser Gly Ser Val Leu  
 Lys Asn Ala Met Met Met Gly Ala Asp Leu Tyr Glu Thr Glu Asp Glu  
 Ile Ser Gly Leu Leu Ser Glu Lys Val Pro Ile Gly Val Gly Glu  
 Asn Ser Lys Leu Ser Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly  
 Arg Asp Val Val Ile Ala Asn Ser Glu Gly Val Gln Glu Ala Asp Arg  
 Pro Glu Glu Gly Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys  
 Asn Ala Thr Val Lys Asp Gly Thr Val Val  
 245 250 255  
 260 265 270  
 275 280 285  
 290 295 300  
 305 310 315  
 320 325 330  
 335 340 345  
 350 355 360  
 365 370 375  
 380 385 390  
 395 400 405  
 410 415 420  
 425 430 435  
 440 445 450  
 455 460 465  
 470 475 480  
 485 490 495  
 500 505 510  
 515 520

&lt;210&gt; 73

&lt;211&gt; 522

&lt;212&gt; PRT

&lt;213&gt; Festuca arundinacea

&lt;400&gt; 73

Met Ser Ser Met Gln Phe Ser Ser Val Leu Pro Leu Glu Gly Lys Ala  
 1 5 10 15  
 Cys Val Cys Pro Val Arg Ser Ala Asn Asn Gly Cys Glu Arg Leu Lys  
 20 25 30  
 Val Gly Asp Ser Ser Ser Leu Arg His Glu Met Ala Leu Arg Arg Lys  
 35 40 45  
 Cys Asn Gly Ala Arg Gly Gly Gly Ala Ala Asp Gly Ala Gln Cys Val  
 50 55 60  
 Leu Thr Ser Asp Ala Ser Pro Asp Thr Leu Val Val Arg Ser Ser Phe  
 65 70 75 80  
 Arg Met Asn Tyr Ala Asp Pro Asn Glu Val Ala Ala Val Ile Leu Gly  
 85 90 95  
 Gly Gly Thr Gly Thr Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr  
 100 105 110  
 Pro Ala Val Pro Ile Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met  
 115 120 125  
 Ser Asn Cys Phe Asn Ser Gly Ile Asn Lys Ile Phe Val Met Thr Gln  
 130 135 140  
 Phe Asn Ser Ala Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Gly  
 145 150 155 160  
 Gly Gly Ile Asn Phe Thr Asp Gly Ser Val Glu Val Leu Ala Ala Thr  
 165 170 175  
 Gln Met Pro Gly Glu Ala Ala Gly Trp Phe Arg Gly Thr Ala Asp Ala  
 180 185 190  
 Val Arg Lys Phe Ile Trp Val Leu Glu Asp Tyr Tyr Lys His Lys Ser  
 195 200 205

Ile Glu His Ile Leu Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asp  
 210 215 220  
 Tyr Met Glu Leu Val Gln Lys His Val Asp Asp Asn Ala Asp Ile Thr  
 225 230 235  
 Leu Ser Cys Ala Pro Val Gly Glu Ser Arg Ala Ser Glu Tyr Gly Leu  
 245 250 255  
 Val Lys Phe Asp Ser Ser Gly Arg Val Ile Gln Phe Ser Glu Lys Pro  
 260 265 270  
 Lys Gly Ala Asp Leu Glu Ala Met Lys Val Asp Thr Ser Phe Leu Asn  
 275 280 285  
 Phe Ala Ile Asp Asp Pro Ala Lys Asn Pro Tyr Ile Ala Ser Met Gly  
 290 295 300  
 Val Tyr Val Phe Lys Arg Glu Val Leu Leu Asn Leu Leu Lys Ser Arg  
 305 310 315  
 Tyr Thr Glu Leu His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Leu  
 325 330 335  
 His Asp His Asn Val Gln Ala Tyr Val Phe Thr Asp Tyr Trp Glu Asp  
 340 345 350  
 Ile Gly Thr Ile Arg Ser Phe Phe Asp Ala Asn Met Ala Leu Cys Glu  
 355 360 365  
 Gln Pro Pro Lys Phe Glu Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr  
 370 375 380  
 Ser Pro Arg Tyr Leu Pro Pro Thr Lys Ser Asp Lys Cys Arg Ile Lys  
 385 390 395  
 Glu Ala Ile Ile Ser His Gly Cys Phe Leu Arg Glu Cys Thr Ile Glu  
 405 410 415  
 His Ser Ile Ile Gly Val Arg Ser Arg Leu Asn Ser Gly Ser Val Leu  
 420 425 430  
 Lys Asn Ala Met Met Met Gly Ala Asp Leu Tyr Glu Thr Glu Asp Glu  
 435 440 445  
 Ile Ser Gly Leu Leu Ser Glu Gly Lys Val Pro Ile Gly Val Gly Glu  
 450 455 460  
 Asn Ser Lys Leu Ser Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly  
 465 470 475  
 Arg Asp Val Val Ile Ala Asn Ser Glu Gly Val Gln Glu Ala Asp Arg  
 485 490 495  
 Pro Glu Glu Gly Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys  
 500 505 510  
 Asn Ala Thr Val Lys Asp Gly Thr Val Val  
 515 520

<210> 74  
 <211> 525  
 <212> PRT  
 <213> Lolium perenne

<400> 74  
 Met Thr Gly Ala Pro Pro Ser Thr Val Met Ala Met Gly Ala Ala Thr  
 1 5 10 15  
 Ser Pro Cys Lys Ile Leu Ser Ala Thr Gln Arg Ala Ser Thr Ala Ala  
 20 25 30  
 Ala Ser Ala Ser Thr Ser Arg Glu Ser Val Ser Leu Arg Ala Pro Arg  
 35 40 45  
 Gly Arg Arg Gln Arg Pro Arg Pro Arg Gly Leu Ala Leu Ser Leu Ala  
 50 55 60  
 Pro Ala Arg Arg Pro Phe Val Phe Ser Pro Arg Ala Val Ser Asp Ser  
 65 70 75 80  
 Lys Ser Ser Gln Thr Cys Leu Asp Pro Asp Ala Ser Thr Ser Val Leu  
 85 90 95  
 Gly Ile Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr  
 100 105 110  
 Lys Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu  
 115 120 125  
 Ile Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile  
 130 135 140  
 Tyr Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser  
 145 150 155 160  
 Arg Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val  
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Glu Val Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln  
 Gly Thr Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His  
 Asn Val Met Glu Tyr Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met  
 Asp Tyr Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asp Ala Asp Ile  
 Thr Val Ala Ala Leu Pro Met Asp Glu Glu Arg Ala Thr Ala Phe Gly  
 Leu Met Lys Ile Asp Glu Glu Gly Arg Ile Val Glu Phe Ala Glu Lys  
 Pro Lys Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu  
 Gly Leu Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met  
 Gly Ile Tyr Val Ile Ser Lys His Val Met Leu Gln Leu Leu Arg Asp  
 Gln Phe Pro Gly Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala  
 Thr Ser Thr Gly Met Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp  
 Glu Asp Ile Gly Thr Ile Glu Ala Phe Tyr Asn Ala Asn Leu Gly Ile  
 Thr Lys Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Ser Ala Pro  
 Ile Tyr Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala  
 Asp Val Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys  
 Lys Ile His His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly  
 Ala Ile Ile Glu Asp Thr Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr  
 Glu Ala Asp Lys Lys Leu Leu Ala Asp Lys Gly Ile Pro Ile Gly  
 Ile Gly Lys Asn Ser His Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala  
 Arg Ile Gly Asp Asn Val Lys Ile Ile Asn Val Asp Asn Val Gln Glu  
 Ala Ala Arg Glu Thr Asp Gly Tyr Phe Ile Lys Ser Gly Ile Val Thr  
 Val Ile Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile

&lt;210&gt; 75

&lt;211&gt; 524

&lt;212&gt; PRT

&lt;213&gt; Festuca arundinacea

&lt;400&gt; 75

Met Thr Arg Ala Pro Pro Ser Thr Val Met Ala Met Gly Ala Ala Thr  
 Ser Pro Cys Lys Ile Leu Ser Ala Thr Gln Arg Ala Ser Ala Ala Ala  
 Pro Ser Ala Ser Thr Ser Arg Glu Ser Val Cys Leu Leu Arg Ala Pro  
 Arg Gly Arg Arg Gln Arg Pro Arg Gly Leu Ala Leu Ser Leu Ala Pro  
 Ala Arg Arg Pro Phe Val Phe Ser Pro Arg Ala Val Ser Asp Ser Lys  
 Ser Ser Gln Thr Cys Leu Asp Pro Asp Ala Ser Thr Ser Val Leu Gly  
 Ile Ile Leu Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys  
 Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile



Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr  
 130 135 140  
 Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg  
 145 150 155  
 Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu  
 165 170  
 Val Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly  
 180 185  
 Thr Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn  
 195 200  
 Val Met Glu Tyr Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp  
 210 215  
 Tyr Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asp Ala Asp Ile Thr  
 225 230  
 Val Ala Ala Leu Pro Met Asp Glu Glu Arg Ala Thr Ala Phe Gly Leu  
 245 250  
 Met Lys Ile Asp Glu Glu Gly Arg Ile Val Glu Phe Ala Glu Lys Pro  
 260 265  
 Lys Gly Glu Gln Leu Lys Ala Met Val Asp Thr Thr Ile Leu Gly  
 275 280  
 Leu Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly  
 290 295  
 Ile Tyr Val Ile Ser Lys His Val Met Leu Gln Leu Leu Arg Asp Gln  
 305 310  
 Phe Pro Gly Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr  
 325 330  
 Ser Thr Gly Met Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu  
 340 345  
 Asp Ile Gly Thr Ile Glu Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr  
 355 360  
 Lys Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Ser Ala Pro Ile  
 370 375  
 Tyr Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp  
 385 390  
 Val Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys  
 405 410  
 Ile His His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala  
 420 425  
 Ile Ile Glu Asp Thr Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu  
 435 440  
 Ala Asp Lys Lys Leu Leu Ala Asp Lys Gly Gly Ile Pro Ile Gly Ile  
 450 455  
 Gly Lys Asn Ser His Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg  
 465 470  
 Ile Gly Asp Asn Val Lys Ile Ile Asn Val Asp Asn Val Gln Glu Ala  
 485 490  
 Ala Arg Glu Thr Asp Gly Tyr Phe Ile Lys Ser Gly Ile Val Thr Val  
 500 505  
 Ile Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile  
 515 520

&lt;210&gt; 76

&lt;211&gt; 398

&lt;212&gt; PRT

&lt;213&gt; Festuca arundinacea

&lt;400&gt; 76

Met Ala Ala Thr Met Thr Val Glu Glu Val Arg Lys Ala Gln Arg Ala  
 1 5 10 15  
 Glu Gly Pro Ala Thr Val Leu Ala Ile Gly Thr Ala Thr Pro Ala Asn  
 20 25  
 Cys Val Tyr Gln Ala Asp Tyr Pro Asp Tyr Tyr Phe Lys Ile Thr Lys  
 35 40 45  
 Ser Asp His Leu Ala Asp Leu Lys Glu Lys Phe Lys Arg Met Cys Asp  
 50 55 60  
 Lys Ser Gln Ile Arg Lys Arg Tyr Met His Leu Thr Glu Glu Ile Leu  
 65 70 75 80  
 Glu Glu Asn Pro Asn Met Cys Ala Tyr Met Ala Pro Ser Leu Asp Ala

Arg	Gln	Asp	Ile	Val	Val	Val	Glu	Val	Pro	Lys	Leu	Gly	Lys	Ala	Ala
Ala	Gln	Lys	Ala	Ile	Lys	Glu	Trp	Gly	Gln	Pro	Arg	Ser	Lys	Ile	Thr
His	Leu	Val	Phe	Cys	Thr	Thr	Ser	Gly	Val	Asp	Met	Pro	Gly	Ala	Asp
Tyr	Gln	Leu	Thr	Lys	Met	Leu	Gly	Leu	Arg	Pro	Ser	Val	Lys	Arg	Leu
Met	Met	Tyr	Gln	Gln	Gly	Cys	Phe	Ala	Gly	Gly	Thr	Val	Leu	Arg	Leu
Ala	Lys	Asp	Leu	Ala	Glu	Asn	Asn	Arg	Gly	Ala	Arg	Val	Leu	Val	Val
Cys	Ser	Glu	Ile	Thr	Ala	Val	Thr	Phe	Arg	Gly	Pro	His	Glu	Ser	His
Leu	Asp	Ser	Leu	Val	Gly	Gln	Ala	Leu	Phe	Gly	Asp	Gly	Ala	Ala	Ala
Val	Ile	Ile	Gly	Ala	Asp	Pro	Asp	Val	Ser	Val	Glu	Arg	Pro	Leu	Phe
Gln	Leu	Val	Ser	Val	Ser	Gln	Thr	Ile	Leu	Pro	Asp	Ser	Glu	Gly	Ala
Ile	Asp	Gly	His	Leu	Arg	Glu	Val	Gly	Leu	Thr	Phe	His	Leu	Leu	Lys
Asp	Val	Pro	Gly	Leu	Ile	Ser	Lys	Asn	Ile	Glu	Arg	Ala	Leu	Glu	Glu
Ala	Phe	Lys	Pro	Leu	Gly	Ile	Asp	Asp	Trp	Asn	Ser	Val	Phe	Trp	Val
Ala	His	Pro	Gly	Gly	Pro	Ala	Ile	Leu	Asp	Met	Val	Glu	Ala	Lys	Val
Asn	Leu	Asn	Lys	Glu	Arg	Met	Arg	Ala	Thr	Arg	His	Val	Leu	Ser	Glu
Tyr	Gly	Asn	Met	Ser	Ser	Ala	Cys	Val	Leu	Phe	Ile	Met	Asp	Glu	Met
Arg	Lys	Arg	Ser	Ala	Glu	Asp	Gly	His	Thr	Thr	Thr	Gly	Glu	Gly	Met
Asp	Trp	Gly	Val	Leu	Phe	Gly	Phe	Gly	Pro	Gly	Leu	Thr	Val	Glu	Thr
Val	Val	Leu	His	Ser	Met	Pro	Ile	Ala	Ala	Asp	Ala	Thr	Ala		

<210> 77  
 <211> 398  
 <212> PRT  
 <213> Festuca arundinacea

Met	Ala	Thr	Thr	Met	Thr	Val	Glu	Glu	Val	Arg	Lys	Ala	Gln	Arg	Ala
Glu	Gly	Pro	Ala	Thr	Val	Leu	Ala	Ile	Gly	Thr	Ala	Thr	Pro	Ala	Asn
Cys	Val	Tyr	Gln	Ala	Asp	Tyr	Pro	Asp	Tyr	Tyr	Phe	Lys	Ile	Thr	Lys
Ser	Asp	His	Leu	Ala	Asp	Leu	Lys	Glu	Lys	Phe	Lys	Arg	Met	Cys	Asp
Lys	Ser	Gln	Ile	Arg	Lys	Arg	Tyr	Met	His	Leu	Thr	Glu	Glu	Ile	Leu
Glu	Glu	Asn	Pro	Asn	Met	Cys	Ala	Tyr	Met	Ala	Pro	Ser	Leu	Asp	Ala
Arg	Gln	Asp	Ile	Val	Val	Val	Glu	Val	Pro	Lys	Leu	Gly	Lys	Ala	Ala
Ala	Gln	Lys	Ala	Ile	Lys	Glu	Trp	Gly	Gln	Pro	Arg	Ser	Lys	Ile	Thr
His	Leu	Val	Phe	Cys	Thr	Thr	Ser	Gly	Val	Asp	Met	Pro	Gly	Ala	Asp
Tyr	Gln	Leu	Thr	Lys	Met	Leu	Gly	Leu	Arg	Pro	Ser	Val	Lys	Arg	Leu
Met	Met	Tyr	Gln	Gln	Gly	Cys	Phe	Ala	Gly	Gly	Thr	Val	Leu	Arg	Leu

Ala Lys Asp Leu Ala Glu Asn Asn Arg Gly Ala Arg Val Leu Val Val  
 180 185 190  
 Cys Ser Glu Ile Thr Ala Val Thr Phe Arg Gly Pro His Glu Ser His  
 195 200 205  
 Leu Asp Ser Leu Val Gly Gln Ala Leu Phe Gly Asp Gly Ala Ala Ala  
 210 215 220  
 Val Ile Ile Gly Ala Asp Pro Asp Val Ser Val Glu His Pro Leu Phe  
 225 230 235 240  
 Gln Leu Val Ser Ala Ser Gln Thr Ile Leu Pro Asp Ser Glu Gly Ala  
 245 250 255  
 Ile Asp Gly His Leu Arg Glu Val Gly Leu Thr Phe His Leu Leu Lys  
 260 265 270  
 Asp Val Pro Gly Leu Ile Ser Lys Asn Ile Glu Arg Ala Leu Glu Glu  
 275 280 285  
 Ala Phe Lys Pro Leu Gly Ile Asp Asp Trp Asn Ser Val Phe Trp Val  
 290 295 300  
 Ala His Pro Gly Gly Pro Ala Ile Leu Asp Met Val Glu Ala Lys Val  
 305 310 315 320  
 Asn Leu Asn Lys Glu Arg Met Arg Ala Thr Arg His Val Leu Ser Glu  
 325 330 335  
 Tyr Gly Asn Met Ser Ser Ala Cys Val Leu Phe Ile Met Asp Glu Met  
 340 345 350  
 Arg Lys Arg Ser Ala Glu Asp Gly His Thr Thr Thr Gly Glu Gly Met  
 355 360 365  
 Asp Trp Gly Val Leu Phe Gly Phe Gly Pro Gly Leu Thr Val Glu Thr  
 370 375 380  
 Val Val Leu His Ser Met Pro Ile Ala Ala Gly Ala Thr Ala  
 385 390 395

&lt;210&gt; 78

&lt;211&gt; 277

&lt;212&gt; PRT

&lt;213&gt; Festuca arundinacea

&lt;400&gt; 78

Arg Ala Asp Leu Glu Glu Gly Ser Phe Asp Asp Ala Val Ala Gly  
 1 5 10 15  
 Cys Asp Tyr Ala Phe Leu Val Ala Ala Pro Val Asn Leu Lys Ala Glu  
 20 25 30  
 Asn Pro Glu Lys Asp Met Val Glu Pro Ala Val Gly Gly Thr Leu Asn  
 35 40 45  
 Ala Met Arg Ser Cys Val Arg Ala Gly Thr Val Lys Arg Val Val Leu  
 50 55 60  
 Thr Ser Ser Val Ala Ser Val Ser Ala Arg Pro Leu Leu Gln Gly Asp  
 65 70 75 80  
 Gly His Val Leu Asp Glu Glu Ser Trp Ser Asp Val Asp Phe Leu Arg  
 85 90 95  
 Ala Lys Ala Thr Gly His Trp Gly Tyr Pro Val Ser Lys Val Leu Leu  
 100 105 110  
 Glu Lys Ala Ala Cys Ala Phe Ala Gln Ala Ser Gly Ile Ser Leu Val  
 115 120 125  
 Thr Val Cys Pro Val Val Val Val Gly Lys Ala Pro Ala Val Gln Val  
 130 135 140  
 His Thr Ser Val Pro Asp Val Leu Ser Pro Leu Ser Gly Asp Glu Ala  
 145 150 155 160  
 Lys Ile Gln Ile Leu Gln His Ile Glu Arg Ala Ser Gly Ser Ile Ser  
 165 170 175  
 Leu Val His Val Asp Asp Leu Cys Arg Ala Glu Val Phe Leu Ala Glu  
 180 185 190  
 Glu Glu Ala Val Ala Ser Gly Arg Tyr Ile Cys Cys Ser Leu Ser Thr  
 195 200 205  
 Thr Ala Gly Val Leu Ala Arg Phe Leu Ser Val Lys Tyr Pro Gln Tyr  
 210 215 220  
 Lys Val Arg Thr Asp Arg Phe Ser Gly Ser Pro Glu Lys Pro Arg Val  
 225 230 235 240  
 Cys Met Ser Ser Ala Lys Leu Val Ala Glu Gly Phe Gln Tyr Lys Tyr  
 245 250 255  
 Lys Thr Leu Asp Glu Ile Tyr Asp Asp Val Val Glu Tyr Gly Arg Ala

Leu Gly Ile 260  
275 Leu Pro 265 270

<210> 79  
<211> 342  
<212> PRT  
<213> Festuca arundinacea

<400> 79  
Met Ala Ala Ala Gly Asp Gly Ser Arg Arg Lys Thr Ala Cys Val Thr  
1 5 10 15  
Gly Gly Asn Gly Tyr Ile Ala Ser Ala Leu Val Lys Met Leu Leu Glu  
20 25 30  
Lys Gly Tyr Ala Val Lys Thr Thr Val Arg Asn Pro Asp Asp Met Glu  
35 40 45  
Lys Asn Ser His Leu Lys Asp Leu Gln Ala Leu Gly Pro Leu Glu Val  
50 55 60  
Phe Arg Ala Asp Leu Gln Glu Glu Gly Ser Phe Asp Asp Ala Val Ala  
65 70 75 80  
Gly Cys Asp Tyr Ala Phe Leu Val Ala Ala Pro Val Asn Leu Lys Ala  
85 90 95  
Glu Asn Pro Glu Lys Asp Met Val Glu Pro Ala Val Gly Gly Thr Leu  
100 105 110  
Asn Ala Met Arg Ser Cys Val Arg Ala Gly Thr Val Lys Arg Val Val  
115 120 125  
Leu Thr Ser Ser Val Ala Ser Val Ser Ala Arg Pro Leu Leu Gln Gly  
130 135 140  
Asp Gly His Val Leu Asp Glu Glu Ser Trp Ser Asp Val Asp Phe Leu  
145 150 155 160  
Arg Ala Lys Ala Thr Gly His Trp Gly Tyr Pro Val Ser Lys Val Leu  
165 170 175  
Leu Glu Lys Ala Cys Ala Phe Ala Gln Ala Ser Gly Ile Ser Leu  
180 185 190  
Val Thr Val Cys Pro Val Val Val Gly Lys Ala Pro Ala Val Gln  
195 200 205  
Val His Thr Ser Val Pro Asp Val Leu Ser Pro Leu Ser Gly Asp Glu  
210 215 220  
Ala Lys Ile Gln Ile Leu Gln His Ile Glu Arg Ala Ser Gly Ser Ile  
225 230 235 240  
Ser Leu Val His Val Asp Asp Leu Cys Arg Ala Glu Val Phe Leu Ala  
245 250 255  
Glu Glu Glu Ala Val Ala Ser Gly Arg Tyr Ile Cys Cys Ser Leu Ser  
260 265 270  
Thr Thr Ala Gly Val Leu Ala Arg Phe Leu Ser Val Lys Tyr Pro Gln  
275 280 285  
Tyr Lys Val Arg Thr Asp Arg Phe Ser Gly Ser Pro Glu Lys Pro Arg  
290 295 300  
Val Cys Met Ser Ser Ala Lys Leu Val Ala Glu Gly Phe Gln Tyr Lys  
305 310 315 320  
Tyr Lys Thr Leu Asp Glu Ile Tyr Asp Asp Val Val Glu Tyr Gly Arg  
325 330 335  
Ala Leu Gly Ile Leu Pro 340

<210> 80  
<211> 255  
<212> PRT  
<213> Lolium perenne

<400> 80  
Phe Ile Ser Val Thr Val Phe Tyr Val Val Gly Leu Arg Gln Arg Asp  
1 5 10 15  
Leu Val Gln Ala Gly Val Gln Gly Thr Leu Asn Val Met Arg Ser Cys  
20 25 30  
Val Lys Ala Gly Thr Val Lys Arg Val Ile Leu Thr Ser Ser Asp Ser  
35 40 45  
Ala Val Cys Gln Arg Pro Leu Glu Gly Asp Gly His Val Leu Asp Glu  
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50 55 60  
 Gly Ser Trp Ser Asp Val Pro Tyr Leu Arg Ala Glu Gln Pro Glu Ala  
 65 70 75 80  
 Trp Gly Tyr Ala Val Ser Lys Val Leu Met Glu Glu Ala Ala Gly Lys  
 85 90 95  
 Phe Ala Asp Glu Asn Gly Leu Gly Leu Val Ser Val Leu Pro Thr Phe  
 100 105 110  
 Thr Leu Gly Ala Ala Pro Val Ser Gln Ala Arg Thr Ser Val Pro Val  
 115 120 125  
 Val Leu Ser Leu Leu Ser Gly Asp Glu Glu Gln Leu Asn Leu Leu Glu  
 130 135 140  
 Ala Met His Leu Ile Thr Glu Ser Val Ser Ile Asn His Ile Asp Asp  
 145 150 155 160  
 Leu Cys Arg Ala Gln Val Phe Leu Ala Glu Asn Glu Ala Ser Ser Gly  
 165 170 175  
 Arg Tyr Ile Cys Ser Ser His Asp Thr Thr Val Val Gln Leu Ala Arg  
 180 185 190  
 Leu Leu Ala Asp Lys Tyr Pro Gln Tyr Asn Val Lys Ser Gln Arg Phe  
 195 200 205  
 Asp Gly Ser Pro Glu Lys Pro Arg Val Cys Leu Ser Ser Gln Lys Leu  
 210 215 220  
 Ile Gly Glu Gly Phe Val Tyr Lys Tyr Asp Asp Leu Gly Ala Ile Leu  
 225 230 235 240  
 Asp Asp Leu Val Glu Tyr Gly Arg Thr Thr Gly Ile Leu Pro Phe  
 245 250 255

<210> 81  
 <211> 340  
 <212> PRT  
 <213> Lolium perenne

<400> 81  
 Met Ala Ser Ala Ala Gly Gly Arg Arg Lys Thr Ala Cys Val Thr Gly  
 1 5 10 15  
 Gly Ser Gly Tyr Ile Ala Ser Ala Leu Ile Lys Thr Leu Leu Asp His  
 20 25 30  
 Gly Tyr Ala Val Lys Thr Thr Val Arg Asn Pro Asp Asp Leu Glu Lys  
 35 40 45  
 Thr Ser His Leu Lys Asp Leu Gln Ala Phe Gly Pro Leu Glu Ile Phe  
 50 55 60  
 Arg Gly Glu Leu Asp Val Glu Gly Ser Phe Asp Asp Ser Val Ser Gly  
 65 70 75 80  
 Cys Asp Tyr Val Phe Leu Val Ala Ala Pro Met Asp Met Gly Ser Leu  
 85 90 95  
 Asn Pro Glu Arg Asp Leu Val Gln Ala Gly Val Gln Gly Thr Leu Asn  
 100 105 110  
 Val Met Arg Ser Cys Val Lys Ala Gly Thr Val Lys Arg Val Ile Leu  
 115 120 125  
 Thr Ser Ser Asp Ser Ala Val Cys Gln Arg Pro Leu Glu Gly Asp Gly  
 130 135 140  
 His Val Leu Asp Glu Gly Ser Trp Ser Asp Val Pro Tyr Leu Arg Ala  
 145 150 155 160  
 Glu Gln Pro Glu Ala Trp Gly Tyr Ala Val Ser Lys Val Leu Met Glu  
 165 170 175  
 Glu Ala Ala Gly Lys Phe Ala Asp Glu Asn Gly Leu Gly Leu Val Ser  
 180 185 190  
 Val Leu Pro Thr Phe Thr Leu Gly Ala Ala Pro Val Ser Gln Ala Arg  
 195 200 205  
 Thr Ser Val Pro Val Val Leu Ser Leu Leu Ser Gly Asp Glu Glu Gln  
 210 215 220  
 Leu Asn Leu Leu Glu Ala Met His Leu Ile Thr Glu Ser Val Ser Ile  
 225 230 235 240  
 Asn His Ile Asp Asp Leu Cys Arg Ala Gln Val Phe Leu Ala Glu Asn  
 245 250 255  
 Glu Ala Ser Ser Gly Arg Tyr Ile Cys Ser Ser His Asp Thr Thr Val  
 260 265 270  
 Val Gln Leu Ala Arg Leu Leu Ala Asp Lys Tyr Pro Gln Tyr Asn Val  
 275 280 285

Lys Ser Gln Arg Phe Asp Gly Ser Pro Glu Lys Pro Arg Val Cys Leu  
 290 295 300  
 Ser Ser Gln Lys Leu Ile Gly Glu Gly Phe Val Tyr Lys Tyr Asp Asp  
 305 310 315 320  
 Leu Gly Ala Ile Leu Asp Asp Leu Val Glu Tyr Gly Arg Thr Thr Gly  
 325 330 335  
 Ile Leu Pro Phe  
 340

<210> 82  
 <211> 508  
 <212> PRT  
 <213> Lolium perenne

<400> 82  
 Ala Ala Ala Ser Ile Trp Phe Leu Phe Arg Gly Ser Ser Ser Gly Lys  
 1 5 10 15  
 Lys Leu Ser Lys Leu Pro Leu Pro Pro Gly Pro Arg Gly Trp Pro Val  
 20 25 30  
 Leu Gly Asn Leu Pro Gln Val Gly Ala Lys Pro His His Thr Met Ala  
 35 40 45  
 Ala Leu Ser Gln Gln Phe Gly Pro Leu Phe Arg Leu Arg Phe Gly Val  
 50 55 60  
 Ala Glu Val Val Val Ala Ala Ser Ala Lys Val Ala Ser Gln Phe Leu  
 65 70 75 80  
 Arg Ala His Asp Ala Asn Phe Ser Asp Arg Pro Pro Asn Ser Gly Ala  
 85 90 95  
 Glu His Val Ala Tyr Asn Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly  
 100 105 110  
 Ser Arg Trp Arg Ala Leu Arg Lys Leu Cys Ala Leu His Leu Phe Ser  
 115 120 125  
 Ala Lys Ala Leu Asp Ala Leu Arg Ala Val Arg Glu Ala Glu Val Ala  
 130 135 140  
 Leu Met Val Lys Gln Leu Lys Glu Ser Ala Pro Ala Gly Val Val Val  
 145 150 155 160  
 Gly Gln Glu Ala Asn Val Cys Ala Thr Asn Ala Leu Ala Arg Ala Ala  
 165 170 175  
 Val Gly Arg Arg Val Phe Gly Gly Ser Ala Gly Glu Gly Ala Arg Glu  
 180 185 190  
 Phe Lys Asp Met Val Val Glu Leu Met Gln Leu Ala Gly Val Phe Asn  
 195 200 205  
 Ile Gly Asp Phe Val Pro Ala Leu Arg Trp Leu Asp Pro Gln Gly Val  
 210 215 220  
 Val Ala Arg Met Lys Arg Leu His Arg Arg Tyr Asp Ala Met Met Asp  
 225 230 235 240  
 Gly Phe Ile Ser Glu Arg Asp Gln Arg His Asn Gln Ala Ala Ala Asp  
 245 250 255  
 Gly Glu Arg Lys Asp Leu Leu Ser Val Met Leu Gly Tyr Met Arg Pro  
 260 265 270  
 Asp Gly Gly Gly Glu Glu Glu Gly Ile Ser Phe Asn His Thr Asp  
 275 280 285  
 Ile Lys Ala Leu Leu Leu Asn Leu Phe Thr Ala Gly Thr Asp Thr Thr  
 290 295 300  
 Ser Ser Thr Val Glu Trp Ala Leu Ala Glu Leu Ile Arg His Lys Asp  
 305 310 315 320  
 Val Leu Thr Gln Ala Gln Arg Glu Leu Asp Asp Ile Val Gly Gln Asp  
 325 330 335  
 Arg Leu Val Thr Glu Ser Asp Leu Pro His Leu Thr Phe Leu Thr Ala  
 340 345 350  
 Val Ile Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro Leu Ser Leu  
 355 360 365  
 Pro Arg Val Ala Thr Glu Asp Cys Glu Val Glu Gly Tyr Arg Ile Pro  
 370 375 380  
 Lys Gly Thr Thr Leu Leu Val Asn Val Trp Ala Ile Ala Arg Asp Pro  
 385 390 395 400  
 Ala Ser Trp Gly Pro Asp Ala Leu Glu Phe Arg Pro Ala Arg Phe Leu  
 405 410 415  
 Ala Gly Gly Leu His Glu Ser Val Asp Val Lys Gly Ser Asp Tyr Glu

Leu Ile Pro 420 Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly 430 Leu Ser Trp  
 Gly Leu 435 Arg Met Val Thr Leu 440 Met Thr Ala Thr Leu 445 Val His Ala Phe  
 Asp Trp Ser Leu Val Asp 455 Gly Leu Thr Pro Glu 460 Lys Leu Asp Met Glu  
 465 Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Ala Pro Leu Met Val Arg  
 Pro Ile Pro Arg 485 Leu Leu Ser Ser Ala 490 Tyr Thr Val 495  
 500 505

<210> 83  
 <211> 524  
 <212> PRT  
 <213> *Lolium perenne*

<400> 83  
 Met Asp His Arg Asp Val Leu Val Leu Leu Cys Ser Leu Ala Ala Leu  
 1 5 10 15  
 Ala Ala Ala Ser Ile Trp Phe Leu Phe Arg Gly Ser Ser Ser Gly Lys  
 20 25 30  
 Lys Leu Ser Lys Leu Pro Leu Pro Pro Gly Pro Arg Gly Trp Pro Val  
 35 40 45  
 Leu Gly Asn Leu Pro Gln Val Gly Ala Lys Pro His Thr Met Ala  
 50 55 60  
 Ala Leu Ser Gln Gln Phe Gly Pro Leu Phe Arg Leu Arg Phe Gly Val  
 65 70 75 80  
 Ala Glu Val Val Val Ala Ala Ser Ala Lys Val Ala Ser Gln Phe Leu  
 85 90 95  
 Arg Ala His Asp Ala Asn Phe Ser Asp Arg Pro Pro Asn Ser Gly Ala  
 100 105 110  
 Glu His Val Ala Tyr Asn Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly  
 115 120 125  
 Ser Arg Trp Arg Ala Leu Arg Lys Leu Cys Ala Leu His Leu Phe Ser  
 130 135 140  
 Ala Lys Ala Leu Asp Ala Leu Arg Ala Val Arg Glu Ala Glu Val Ala  
 145 150 155 160  
 Leu Met Val Lys Gln Leu Lys Glu Ser Ala Pro Ala Gly Val Val Val  
 165 170 175  
 Gly Gln Glu Ala Asn Val Cys Ala Thr Asn Ala Leu Ala Arg Ala Ala  
 180 185 190  
 Val Gly Arg Val Phe Gly Gly Ser Ala Gly Glu Gly Ala Arg Glu  
 195 200 205  
 Phe Lys Asp Met Val Val Glu Leu Met Gln Leu Ala Gly Val Phe Asn  
 210 215 220  
 Ile Gly Asp Phe Val Pro Ala Leu Arg Trp Leu Asp Pro Gln Gly Val  
 225 230 235 240  
 Val Ala Arg Met Lys Arg Leu His Arg Arg Tyr Asp Ala Met Met Asp  
 245 250 255  
 Gly Phe Ile Ser Glu Arg Asp Gln Arg His Asn Gln Ala Ala Ala Asp  
 260 265 270  
 Gly Glu Arg Lys Asp Leu Leu Ser Val Met Leu Gly Tyr Met Arg Pro  
 275 280 285  
 Asp Gly Gly Gly Gly Glu Glu Glu Gly Ile Ser Phe Asn His Thr Asp  
 290 295 300  
 Ile Lys Ala Leu Leu Leu Asn Leu Phe Thr Ala Gly Thr Asp Thr Thr  
 305 310 315 320  
 Ser Ser Thr Val Glu Trp Ala Leu Ala Glu Leu Ile Arg His Lys Asp  
 325 330 335  
 Val Leu Thr Gln Ala Gln Arg Glu Leu Asp Asp Ile Val Gly Gln Asp  
 340 345 350  
 Arg Leu Val Thr Glu Ser Asp Leu Pro His Leu Thr Phe Leu Thr Ala  
 355 360 365  
 Val Ile Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro Leu Ser Leu  
 370 375 380  
 Pro Arg Val Ala Thr Glu Asp Cys Glu Val Glu Gly Tyr Arg Ile Pro  
 385 390 395 400

Lys Gly Thr Thr Leu Leu Val Asn Val Trp Ala Ile Ala Arg Asp Pro  
 405 410 415  
 Ala Ser Trp Gly Pro Asp Ala Leu Glu Phe Arg Pro Ala Arg Phe Leu  
 420 425 430  
 Ala Gly Gly Leu His Glu Ser Val Asp Val Lys Gly Ser Asp Tyr Glu  
 435 440 445  
 Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Leu Ser Trp  
 450 455 460  
 Gly Leu Arg Met Val Thr Leu Met Thr Ala Thr Leu Val His Ala Phe  
 465 470 475 480  
 Asp Trp Ser Leu Val Asp Gly Leu Thr Pro Glu Lys Leu Asp Met Glu  
 485 490 495  
 Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Ala Pro Leu Met Val Arg  
 500 505 510  
 Pro Ile Pro Arg Leu Leu Ser Ser Ala Tyr Thr Val  
 515 520

&lt;210&gt; 84

&lt;211&gt; 525

&lt;212&gt; PRT

&lt;213&gt; Festuca arundinacea

&lt;400&gt; 84

Arg Ser Glu Leu Ala Gly Met Asp Ile Pro Leu Ser Leu Leu Leu Ser  
 1 5 10 15  
 Thr Leu Ala Ile Ser Ala Thr Ile Cys Tyr Val Phe Phe Arg Ala Gly  
 20 25 30  
 Lys Gly His Arg Ala Pro Leu Pro Leu Pro Gly Pro Arg Gly Trp  
 35 40 45  
 Pro Val Leu Gly Asn Leu Pro Gln Leu Gly Gly Lys Thr His Gln Thr  
 50 55 60  
 Leu His Glu Met Thr Lys Val Tyr Gly Pro Val Leu Arg Leu Arg Phe  
 65 70 75 80  
 Gly Ser Ser Val Val Val Val Ala Gly Ser Ala Ala Val Ala Glu Gln  
 85 90 95  
 Phe Leu Arg Thr His Asp Ala Lys Phe Ser Ser Arg Pro Pro Asn Ser  
 100 105 110  
 Gly Gly Glu His Met Ala Tyr Asn Tyr Arg Asp Val Val Phe Ala Pro  
 115 120 125  
 Tyr Gly Pro Arg Trp Arg Ala Met Arg Lys Val Cys Ala Val Asn Ile  
 130 135 140  
 Phe Ser Ala Arg Ala Leu Asp Asp Leu Arg Gly Phe Arg Glu Arg Glu  
 145 150 155 160  
 Ala Ala Leu Met Val Arg Ser Leu Ala Asp Ala Ala Lys Ala Gly Val  
 165 170 175  
 Ala Val Ala Val Gly Lys Ala Ala Asn Val Cys Thr Thr Asn Gly Leu  
 180 185 190  
 Ser Arg Ala Ala Val Gly Leu Arg Val Phe Gly Ser Asp Gly Ala Arg  
 195 200 205  
 Asp Phe Lys Glu Ile Val Leu Glu Val Met Glu Val Gly Gly Val Leu  
 210 215 220  
 Asn Val Gly Asp Phe Val Pro Ala Leu Arg Trp Leu Asp Pro Gln Gly  
 225 230 235 240  
 Val Val Ala Arg Leu Lys Lys Leu His Arg Arg Phe Asp Asp Met Met  
 245 250 255  
 Asn Gly Ile Ile Ala Glu Arg Arg Thr Gly Thr Lys Thr Ala Val Val  
 260 265 270  
 Glu Glu Gly Lys Gly Asp Leu Leu Gly Leu Leu Leu Ala Met Val Gln  
 275 280 285  
 Glu Asp Lys Ser Leu Thr Gly Ser Glu Glu Asp Lys Ile Thr Asp Thr  
 290 295 300  
 Asp Val Lys Ala Leu Ile Leu Asn Leu Phe Val Ala Gly Thr Glu Thr  
 305 310 315 320  
 Thr Ser Ser Ile Val Glu Trp Ala Val Ala Glu Leu Ile Arg His Pro  
 325 330 335  
 Asp Ile Leu Lys Gln Ala Gln Glu Glu Leu Asp Ala Val Val Gly Arg  
 340 345 350  
 Asp Arg Leu Val Ser Glu Ser Asp Leu Pro Arg Leu Thr Phe Phe Asn



Ala Ile 355 Lys Glu Thr Phe 360 Arg Leu His Pro Ser 365 Thr Pro Leu Ser  
 Leu 370 Arg Met Ala Ser 375 Glu Glu Cys Glu Val 380 Ala Gly Tyr His Ile  
 385 Pro Arg Gly Thr Glu 390 Leu Leu Val Asn Val 395 Trp Gly Ile Ala Arg Asp  
 Pro Ala Leu Trp 405 Pro Asp Pro Leu Glu Tyr Gln Pro Ala Arg Phe Leu  
 420 Pro Gly Gly Ser His Glu Asn Val 425 Asp Leu Lys Gly Gly Asp Phe Gly  
 435 Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Leu Ser Trp  
 450 Gly Leu Arg Met Val Thr 455 Ile Thr Thr Ala Thr 460 Leu Val His Ser Phe  
 465 Asp Trp Glu Leu Pro 470 Ala Gly Gln Thr Pro 475 Asp Lys Leu Asn Met Glu  
 Glu Ala Phe Ser 485 Leu Leu Leu Gln Arg 490 Ala Val Pro Leu Met 495 Val His  
 Pro Val Pro 500 Arg Leu Leu Pro Ser 505 Ala Tyr Glu Ile Ser 510  
 515 520 525

&lt;210&gt; 85

&lt;211&gt; 526

&lt;212&gt; PRT

&lt;213&gt; Festuca arundinacea

&lt;400&gt; 85

Met Arg Ser Glu Leu Ala Gly Met Asp Ile Pro Leu Pro Leu Leu Leu  
 1 5 10 15  
 Ser Thr Leu Ala Ile Ser Ala Thr Ile Cys Tyr Val Phe Phe Arg Ala  
 20 25 30  
 Gly Lys Gly His Arg Ala Pro Leu Pro Leu Pro Pro Gly Pro Arg Gly  
 35 40 45  
 Trp Pro Val Leu Gly Asn Leu Pro Gln Leu Gly Gly Lys Thr His Gln  
 50 55 60  
 Thr Leu His Glu Met Thr Lys Val Tyr Gly Pro Val Leu Arg Leu Arg  
 65 70 75 80  
 Phe Gly Ser Ser Val Val Val Ala Gly Ser Ala Ala Val Ala Glu  
 85 90 95  
 Gln Phe Leu Arg Thr His Asp Ala Lys Phe Ser Ser Arg Pro Pro Asn  
 100 105 110  
 Ser Gly Gly Glu His Met Ala Tyr Asn Tyr Arg Asp Val Val Phe Ala  
 115 120 125  
 Pro Tyr Gly Pro Arg Trp Arg Ala Met Arg Lys Val Cys Ala Val Asn  
 130 135 140  
 Ile Phe Ser Ala Arg Ala Leu Asp Asp Leu Arg Gly Phe Arg Glu Arg  
 145 150 155 160  
 Glu Ala Ala Leu Met Val Arg Ser Leu Ala Asp Ala Ala Lys Ala Gly  
 165 170 175  
 Val Ala Val Ala Val Gly Lys Ala Ala Asn Val Cys Thr Thr Asn Gly  
 180 185 190  
 Leu Ser Arg Ala Ala Val Gly Leu Arg Val Phe Gly Ser Asp Gly Ala  
 195 200 205  
 Arg Asp Phe Lys Glu Ile Val Leu Glu Val Met Glu Val Gly Gly Val  
 210 215 220  
 Leu Asn Val Gly Asp Phe Val Pro Ala Leu Arg Trp Leu Asp Pro Gln  
 225 230 235 240  
 Gly Val Val Ala Arg Leu Lys Lys Leu His Arg Arg Phe Asp Asp Met  
 245 250 255  
 Met Asn Gly Ile Ala Glu Arg Arg Thr Gly Thr Lys Thr Ala Val  
 260 265 270  
 Val Glu Glu Gly Lys Gly Asp Leu Leu Gly Leu Leu Ala Met Val  
 275 280 285  
 Gln Glu Asp Lys Ser Leu Thr Gly Ser Glu Glu Asp Lys Ile Thr Asp  
 290 295 300  
 Thr Asp Val Lys Ala Leu Ile Leu Asn Leu Phe Val Ala Gly Thr Glu  
 305 310 315 320

Thr Thr Ser Ser Ile Val Glu Trp Ala Val Ala Glu Leu Ile Arg His  
 Pro Asp Ile Leu Lys Gln Ala Gln Glu Glu Leu Asp Ala Val Val Gly  
 Arg Asp Arg Leu Val Ser Glu Ser Asp Leu Pro Arg Leu Thr Phe Phe  
 Asn Ala Ile Ile Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro Leu  
 Ser Leu Pro Arg Met Ala Ser Glu Glu Cys Glu Val Ala Gly Tyr His  
 Ile Pro Arg Gly Thr Glu Leu Leu Val Asn Val Trp Gly Ile Ala Arg  
 Asp Pro Ala Leu Trp Pro Asp Pro Leu Glu Tyr Gln Pro Ala Arg Phe  
 Leu Pro Gly Gly Ser His Glu Asn Val Asp Leu Lys Gly Gly Asp Phe  
 Gly Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Leu Ser  
 Trp Gly Leu Arg Met Val Thr Ile Thr Thr Ala Thr Leu Val His Ser  
 Phe Asp Trp Glu Leu Pro Ala Gly Gln Thr Thr Pro Asp Lys Leu Asn Met  
 Glu Glu Ala Phe Ser Leu Leu Leu Gln Arg Ala Val Pro Leu Met Val  
 His Pro Val Pro Arg Leu Leu Pro Ser Ala Tyr Glu Ile Ser

<210> 86  
 <211> 491  
 <212> PRT  
 <213> Festuca arundinacea

<400> 86  
 Asp Ile Pro Leu Pro Leu Leu Leu Ser Thr Leu Ala Ile Ser Ala Thr  
 Ile Cys Tyr Val Phe Phe Arg Ala Gly Lys Thr His Gln Thr Leu His  
 Glu Met Thr Lys Val Tyr Gly Pro Val Leu Arg Leu Arg Phe Gly Ser  
 Ser Val Val Val Val Ala Gly Ser Ala Ala Val Ala Glu Gln Phe Leu  
 Arg Thr His Asp Ala Lys Phe Ser Ser Arg Pro Asn Ser Gly Gly  
 Glu His Met Ala Tyr Asn Tyr Gln Asp Ile Val Phe Ala Pro Tyr Gly  
 Pro Arg Trp Arg Ala Met Arg Lys Val Cys Ala Val Asn Ile Phe Ser  
 Ala Arg Ala Leu Asp Asp Leu Arg Gly Phe Arg Glu Arg Glu Ala Ala  
 Leu Met Val Arg Ser Leu Ala Asp Ala Ala Lys Ala Gly Ala Ala Val  
 Ala Val Gly Lys Ala Ala Asn Val Cys Thr Thr Asn Gly Leu Ser Arg  
 Ala Ala Val Gly Leu Arg Val Phe Gly Ser Asp Gly Thr Arg Asp Phe  
 Lys Glu Ile Val Leu Glu Val Met Glu Val Gly Gly Val Leu Asn Val  
 Gly Asp Phe Val Pro Ala Leu Arg Trp Leu Asp Pro Gln Gly Val Val  
 Ala Arg Met Lys Lys Leu His Arg Arg Phe Asp Asp Ile Met Asn Gly  
 Ile Ile Ala Glu Arg Arg Thr Gly Ala Lys Thr Ala Val Val Glu Glu  
 Gly Lys Gly Asp Leu Leu Gly Leu Leu Leu Ala Met Val Gln Glu Asp  
 Lys Ser Leu Thr Gly Ser Glu Glu Asp Lys Ile Thr Asp Thr Asp Val  
 Lys Ala Leu Ile Leu Asn Leu Phe Val Ala Gly Thr Glu Thr Thr Ser

Ser Ile Val Glu Trp Ala Val Ala Glu Leu Ile Arg His Pro Asp Ile  
 275 280 285  
 290 295 300  
 Leu Lys Gln Ala Gln Glu Leu Asp Thr Val Val Gly Arg Asp Arg  
 305 310 315  
 Ile Val Ser Glu Ser Asp Leu Pro Arg Leu Thr Phe Phe Asn Ala Ile  
 325 330 335  
 Ile Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro Leu Ser Leu Pro  
 340 345 350  
 Arg Met Ala Ser Glu Asp Cys Glu Val Ala Gly Tyr His Ile Pro Arg  
 355 360 365  
 Gly Thr Glu Leu Leu Val Asn Val Trp Gly Ile Ala Arg Asp Pro Ser  
 370 375 380  
 Leu Trp Pro Asp Pro Leu Glu Tyr Arg Pro Ala Arg Phe Leu Pro Gly  
 385 390 395  
 Gly Ser His Glu Asn Val Asp Leu Lys Gly Gly Asp Phe Gly Leu Ile  
 405 410 415  
 Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Leu Ser Trp Gly Leu  
 420 425 430  
 Arg Met Val Thr Val Thr Thr Ala Thr Leu Val His Ser Phe Asp Trp  
 435 440 445  
 Glu Leu Pro Ala Gly Gln Thr Leu Asp Lys Leu Asn Met Glu Glu Ala  
 450 455 460  
 Phe Ser Leu Leu Leu Gln Arg Ala Met Pro Leu Met Val His Pro Val  
 465 470 475 480  
 Pro Arg Leu Leu Pro Ser Ala Tyr Glu Ile Ser  
 485 490

&lt;210&gt; 87

&lt;211&gt; 499

&lt;212&gt; PRT

&lt;213&gt; Festuca arundinacea

&lt;400&gt; 87

Met Arg Asn Glu Leu Ala Gly Met Asp Ile Pro Leu Pro Leu Leu Leu  
 1 5 10 15  
 Ser Thr Leu Ala Ile Ser Ala Thr Ile Cys Tyr Val Phe Phe Arg Ala  
 20 25 30  
 Gly Lys Thr His Gln Thr Leu His Glu Met Thr Lys Val Tyr Gly Pro  
 35 40 45  
 Val Leu Arg Leu Arg Phe Gly Ser Ser Val Val Val Val Ala Gly Ser  
 50 55 60  
 Ala Ala Val Ala Glu Gln Phe Leu Arg Thr His Asp Ala Lys Phe Ser  
 65 70 75 80  
 Ser Arg Pro Pro Asn Ser Gly Gly Glu His Met Ala Tyr Asn Tyr Gln  
 85 90 95  
 Asp Ile Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg Ala Met Arg Lys  
 100 105 110  
 Val Cys Ala Val Asn Ile Phe Ser Ala Arg Ala Leu Asp Asp Leu Arg  
 115 120 125  
 Gly Phe Arg Glu Arg Glu Ala Ala Leu Met Val Arg Ser Leu Ala Asp  
 130 135 140  
 Ala Ala Lys Ala Gly Ala Ala Val Ala Val Gly Lys Ala Ala Asn Val  
 145 150 155 160  
 Cys Thr Thr Asn Gly Leu Ser Arg Ala Ala Val Gly Leu Arg Val Phe  
 165 170 175  
 Gly Ser Asp Gly Thr Arg Asp Phe Lys Glu Ile Val Leu Glu Val Met  
 180 185 190  
 Glu Val Gly Gly Val Leu Asn Val Gly Asp Phe Val Pro Ala Leu Arg  
 195 200 205  
 Trp Leu Asp Pro Gln Gly Val Ala Arg Met Lys Lys Leu His Arg  
 210 215 220  
 Arg Phe Asp Asp Ile Met Asn Gly Ile Ile Ala Glu Arg Arg Thr Gly  
 225 230 235 240  
 Ala Lys Thr Ala Val Val Glu Glu Gly Lys Gly Asp Leu Leu Gly Leu  
 245 250 255  
 Leu Leu Ala Met Val Gln Glu Asp Lys Ser Leu Thr Gly Ser Glu Glu  
 260 265 270

Asp Lys Ile Thr Asp Thr Asp Val Lys Ala Leu Ile Leu Asn Leu Phe  
 275 280  
 Val Ala Gly Thr Glu Thr Thr Ser Ser Ile Val Glu Trp Ala Val Ala  
 290 295 300  
 Glu Leu Ile Arg His Pro Asp Ile Leu Lys Gln Ala Gln Glu Glu Leu  
 305 310 315 320  
 Asp Thr Val Val Gly Arg Asp Arg Ile Val Ser Glu Ser Asp Leu Pro  
 325 330 335  
 Arg Leu Thr Phe Phe Asn Ala Ile Ile Lys Glu Thr Phe Arg Leu His  
 340 345 350  
 Pro Ser Thr Pro Leu Ser Leu Pro Arg Met Ala Ser Glu Asp Cys Glu  
 355 360 365  
 Val Ala Gly Tyr His Ile Pro Arg Gly Thr Glu Leu Leu Val Asn Val  
 370 375 380  
 Trp Gly Ile Ala Arg Asp Pro Ser Leu Trp Pro Asp Pro Leu Glu Tyr  
 385 390 395 400  
 Arg Pro Ala Arg Phe Leu Pro Gly Gly Ser His Glu Asn Val Asp Leu  
 405 410 415  
 Lys Gly Gly Asp Phe Gly Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile  
 420 425 430  
 Cys Ala Gly Leu Ser Trp Gly Leu Arg Met Val Thr Val Thr Thr Ala  
 435 440 445  
 Thr Leu Val His Ser Phe Asp Trp Glu Leu Pro Ala Gly Gln Thr Leu  
 450 455 460  
 Asp Lys Leu Asn Met Glu Glu Ala Phe Ser Leu Leu Leu Gln Arg Ala  
 465 470 475 480  
 Met Pro Leu Met Val His Pro Val Pro Arg Leu Leu Pro Ser Ala Tyr  
 485 490 495  
 Glu Ile Ser

<210> 88  
 <211> 380  
 <212> PRT  
 <213> Lolium perenne

<400> 88  
 Met Ala Met Ala Asp Cys Met Gln Glu Trp Pro Glu Pro Val Val Arg  
 1 5 10 15  
 Val Gln Ala Val Ala Glu Ser Gly Leu Ala Ala Ile Pro Asp Cys Tyr  
 20 25 30  
 Val Lys Pro Pro Arg Asp Arg Pro Ala Ala Gln His Leu Ala Thr Ala  
 35 40 45  
 Ala Ser Ala Asp Gly Asp Val Leu His Glu Pro Leu Asp Thr Ser Ile  
 50 55 60  
 Pro Val Ile Asp Leu Gly Glu Leu Val Ala Ala Thr Ala Asp Glu Gly  
 65 70 75 80  
 Arg Met Arg Gln Ile Met Glu Ala Val Ala Ala Cys Arg Glu Trp  
 85 90 95  
 Gly Phe Phe Gln Val Val Asn His Gly Val Ala Pro Glu Leu Met His  
 100 105 110  
 Ala Ala Arg Glu Ala Trp Arg Gly Phe Phe Arg Leu Pro Ile Thr Ala  
 115 120 125  
 Lys Gln Gln Tyr Ala Asn Leu Pro Arg Thr Tyr Glu Gly Tyr Gly Ser  
 130 135 140  
 Arg Val Gly Val Gln Lys Gly Gly Pro Leu Asp Trp Gly Asp Tyr Tyr  
 145 150 155 160  
 Phe Leu His Leu Ala Pro Asp Ala Gly Lys Ser Pro Asp Lys Tyr Trp  
 165 170 175  
 Pro Thr Asn Pro Ala Ile Cys Lys Asp Val Ser Glu Glu Tyr Gly Arg  
 180 185 190  
 Glu Val Ile Arg Leu Cys Glu Leu Leu Met Lys Val Met Ser Ala Ser  
 195 200 205  
 Leu Gly Leu Glu Ala Thr Arg Phe Gln Glu Ala Phe Gly Gly Ser Glu  
 210 215 220  
 Cys Gly Val Cys Leu Arg Ala Asn Tyr Tyr Pro Arg Cys Pro Gln Pro  
 225 230 235 240  
 Asp Leu Thr Leu Gly Leu Ser Ala His Ser Asp Pro Gly Val Leu Thr

Val Leu Leu Ala<sup>245</sup> Asp Glu His Val Arg Gly<sup>250</sup> Leu Gln Val Arg Arg<sup>255</sup> Ala  
 Asp Gly Glu<sup>260</sup> Trp Val Thr Val Gln<sup>265</sup> Pro Ala Arg His Asp Ala<sup>270</sup> Phe Ile  
 Val Asn Val Gly<sup>275</sup> Asp Gln Ile<sup>280</sup> Gln Ile Leu Ser Asn<sup>285</sup> Ser Met Tyr Lys  
 Ser Val Glu His Arg Val<sup>290</sup> Met Val Asn Ala Lys<sup>295</sup> Glu Glu Arg Ile Ser  
 Leu Ala Leu Phe Tyr<sup>300</sup> Asn Pro Arg Gly Asp Val<sup>305</sup> Pro Ile Ala Pro Ala  
 Pro Glu Thr Val<sup>310</sup> Thr Pro Glu Arg Pro Ala<sup>315</sup> Leu Tyr Pro Ser Met Thr  
 Phe Asp Glu Tyr<sup>320</sup> Arg Ala Tyr Ile<sup>325</sup> Arg Lys Tyr Gly Pro Arg Gly Lys  
 Ala Gln Val<sup>330</sup> Glu Gly Ala Lys<sup>335</sup> Gln Gly Gln Gly Ser  
 370 375 380

<210> 89  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Made in the lab

<400> 89  
 gacgcaagga gagatccaga 20

<210> 90  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Made in the lab

<400> 90  
 agacgaggtg ggtgatcttg 20

<210> 91  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Made in the lab

<400> 91  
 tacatatgaa gagagtttca tcgcat 26

<210> 92  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Made in the lab

<400> 92  
 gccgaacaga ccattgaagt a 21

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/NZ03/00081

**A. CLASSIFICATION OF SUBJECT MATTER**Int. Cl. <sup>7</sup>: C12N 9/10, 9/02, 5/14, 15/82, C07K 14/415, A01H 5/00

According to International Patent Classification (IPC) or to both national classification and IPC

**B. FIELDS SEARCHED**

Minimum documentation searched (classification system followed by classification symbols)

See electronic database box below.

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

See electronic database box below.

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

DGENE, EMBL, GenBank, PDB, DDBJ, USPTO sequences: SEQ ID NO: 4, 12, 15, 15, 17, 20, 22, 27, 33, 35, 37.

**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	EMBL database Accession Number AF492836 & AAM13671. Lasseur B <i>et al.</i> 16 April 2002. "Lolium perenne putative sucrose:sucrose 1-fructosyltransferase mRNA, complete cds". See whole document. 97.8% identical to SEQ ID NOs: 4 and 48.	1-25 (SEQ ID NO: 4 & 48)
X	Luscher M <i>et al.</i> (2000) Plant Physiol. 124(3):1217-28. "Cloning and functional analysis of sucrose:sucrose 1-fructosyltransferase from tall fescue". & EMBL database Accession Number AJ297369 & CAC05261. See whole document. 83% identical to SEQ ID NO: 4 and 48.	1-25 (SEQ ID NO: 4 & 48)

☒ Further documents are listed in the continuation of Box C☒ See patent family annex

* Special categories of cited documents:	
"A" document defining the general state of the art which is not considered to be of particular relevance	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"E" earlier application or patent but published on or after the international filing date	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O" document referring to an oral disclosure, use, exhibition or other means	"&" document member of the same patent family
"P" document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search  
22 August 2003

Date of mailing of the international search report

27 AUG 2003

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## INTERNATIONAL SEARCH REPORT

International application No.

PCT/NZ03/00081

**Box I Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)**

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos :  
because they relate to subject matter not required to be searched by this Authority, namely:
  
2. ☐ Claims Nos :  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
  
3. ☐ Claims Nos :  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a)

**Box II Observations where unity of invention is lacking (Continuation of item 3 of first sheet)**

This International Searching Authority found multiple inventions in this international application, as follows:

See extra sheet below.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims  
☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
  
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:1-25 (in part).

**Remark on Protest**

- ☐ The additional search fees were accompanied by the applicant's protest.  
☐ No protest accompanied the payment of additional search fees.

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/NZ03/00081

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages (Remove spaces when completed if the page is too long)	Relevant to claim No.
X	WO 01/95691, A (State of Victoria, Department of Natural Resources and Environment <i>et al.</i> ) 20 December 2001. See whole document. SST (Figure 11 & SEQ ID NO: 11) is 95% identical to SEQ ID NO: 4.	1-25 (SEQ ID NOs: 4 & 48)
X	WO 02/31130, A (Agriculture Victoria Services Pty Ltd & AGRESEARCH Ltd) 18 April 2002. See whole document. SST (figure 56) is 95% identical to SEQ ID NO: 4. SFT (figure 61) is 98% identical to SEQ ID NO: 4. INV (figure 20) is 64.4% identical to SEQ ID NO: 12. SPS (figures 5, 15 and 17) are 96-99% identical to SEQ ID NO: 20. ST (figures 47 and 49) are 94-96.5% identical to SEQ ID NO: 22.	1-25 (SEQ ID NOs: 4 & 48, 12 & 56, 20 & 64, 22 & 66)
X	US 2001/0051335, A (Lalgudi R V <i>et al.</i> ) 13 December 2001. See whole document. SEQ ID NO: 5640 is 86.4% identical to SEQ ID NO: 12. SEQ ID NOs: 745 & 4804 are 85.7% and 87.5% respectively identical to SEQ ID NO: 15. SEQ ID NO: 5903 is 83.5% identical to SEQ ID NO: 27.	2-4, 6-10, 12, 13. (SEQ ID NO: 12 & 56, 15 & 59, 27 & 71)
X	EP 1033405, A (Ceres Incorporated Malibu) 6 September 2000. See whole document. SEQ ID NO: 11557 is 74% identical to SEQ ID NO: 12. SEQ ID NO: 43076 & 48532 are 81.3% and 73.3 % respectively identical to SEQ ID NO: 17. SEQ ID NO: 20393 is 38.8% identical to SEQ ID NO: 37, also 100% match over 21 nucleotides (nt100-120 of SEQ ID NO: 20393 matches nt555-575 of SEQ ID NO: 37).	2-4, 6-16. (SEQ ID NO: 12 & 56, 17 & 61, 37 & 81)
X	EMBL database Accession Number: AF095521 & AAC67587. Kapri R & Sadka A. 26 October 1998. "Citrus X paradisi pyrophosphate-dependent phosphofructokinase alpha subunit (PPi-PFKa) mRNA, complete cds". See whole document. 70.6% identical to SEQ ID NO: 15 over entire length, 83% identical over 407 nucleotides (nt 634-1040).	1-25. (SEQ ID NO: 15 & 59)
X	Carlisle S M <i>et al.</i> (1990) J Biol. Chem. 265(30): 18366-18371. "Pyrophosphate-dependent phosphofructokinase. Conservation of protein sequence between the alpha- and beta-subunits and with the ATP-dependent phosphofructokinase" & EMBL database Accession Number: M55190 & AAA63451 and M55191 & AAA63452. See whole document. 70.7% identical to SEQ ID NO: 15. 78% identical to SEQ ID NO: 17.	1-25. (SEQ ID NO: 15 & 59, 17 & 61))



## INTERNATIONAL SEARCH REPORT

International application No.

PCT/NZ03/00081

C (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages (Remove spaces when completed if the page is too long)	Relevant to claim No.
X	WO 02/16655, A (The Scripps Research Institute <i>et al.</i> ) 28 February 2002. See whole document. SEQ ID NO: 2691 is 72.2% identical to SEQ ID NO: 15. SEQ ID NO: 188 is 73.3% identical to SEQ ID NO: 17.	1-25 (SEQ ID NO: 15 & 59, 17 & 61)
P, X	US 6476212, B (Lalgudi, R V <i>et al.</i> ) 5 November 2002. See whole document. SEQ ID NO: 584, 1329, 3963, 7175 are 86%, 93%, 87% and 85% identical to SEQ ID NO: 15 respectively.	2-4, 6-14. (SEQ ID NO: 15 & 59)
X	EMBL database Accession Number: AF095520 & AAC67586. Kapri R & Sadka A. 26 October 1998. "Citrus X paradisi pyrophosphate-dependent phosphofructokinase beta subunit (PPi-PFKb) mRNA, complete cds". See whole document. 37.7% identical to SEQ ID NO: 17 over entire length, 82% identical over 620 nucleotides (nt 513-1132 matches nt 541-1160 of SEQ ID NO: 17)	1-25. (SEQ ID NO: 17 & 61)
X	US 2002/0042930, A (Botha F C & Groenewald J H) 11 April 2002. See whole document. Especially figure 2 And SEQ ID NO: 2 83.2% identical to SEQ ID NO: 17.	1-25 (SEQ ID NO: 17 & 61)
P, X	WO 03/000905, A (SYNGENTA PARTICIPATIONS AG) 3 January 2003. See whole document. SEQ ID NO: 179, 587, 1002 are 92%, 87% & 87% identical to SEQ ID NO: 17 respectively.	1-25 (SEQ ID NO: 17 & 61)
X	EMBL database Accession Number: AF261107 & AAF75266. Lunn J E <i>et al.</i> 11 June 2000. "Hordeum vulgare sucrose-phosphate synthase mRNA, partial cds". See whole document. 88.6% identical to SEQ ID NO: 20.	1-25 (SEQ ID NO: 20 & 64)
X	WO 99/57285, A (E.I. DU PONT DE NEMOURS AND COMPANY) 11 November 1999. See whole document. SEQ ID NO: 9 & 19 are 85% & 85.4% identical to SEQ ID NO: 20 respectively.	1-25 (SEQ ID NO: 20 & 64)
X	EMBL database Accession Number: AJ272309 & CAB75882. Weschke W <i>et al.</i> 22 February 2000. "Hordeum vulgare mRNA for sucrose transporter 1 (Sut1 gene)" See whole document. 83.6% identical to SEQ ID NO: 22.	1-25 (SEQ ID NO: 22 & 66)

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/NZ03/00081

C (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages (Remove spaces when completed if the page is too long)	Relevant to claim No.
X	EMBL database Accession Numbers: AF408842, AF408843 & AF408844 (& AAM13408, AAM13409 & AAM13410). Aoki N <i>et al.</i> 16 April 2002. "Triticum aestivum sucrose transporter SUT1A, SUT1B, SUT1D mRNA, complete cds" See whole documents. AF408842 is 82.8% identical to SEQ ID NO: 22. AF408843 is 82.9% identical to SEQ ID NO: 22. AF408844 is 81.8% identical to SEQ ID NO: 22.	1-25 (SEQ ID NO: 22 & 66)
X	WO 99/53068, A ((E.I. DU PONT DE NEMOURS AND COMPANY) 21 October 1999. See whole document, especially SEQ ID NO: 19-22. SEQ ID NO: 19 & 21 are 81.5% & 83% identical to SEQ ID NO: 22.	1-25 (SEQ ID NO: 22 & 66)
X	WO 01/64890, A (Pioneer Hi-Bred International, Inc.) 7 September 2001. See whole document, see SEQ ID NO: 8. SEQ ID NO: 8 is 63.3% identical to SEQ ID NO: 27.	2-4, 6-16 (SEQ ID NO: 27 & 71)
X	EMBL database Accession Number: X92547 & CAA63305. Haussuehl K K <i>et al.</i> 12 August 1996. "S. cereale mRNA for chalcone synthase". See whole document. 85.5% identical to SEQ ID NO: 33.	1-25 (SEQ ID NO: 33 & 77)
X	EMBL database Accession Number: X58339 & CAA41250. Rohde W E <i>et al.</i> 7 November 1991. "H. vulgare CHS gene for chalcone synthase". See whole document. 74.8% identical to SEQ ID NO: 33.	1-25 (SEQ ID NO: 33 & 77)
X	EMBL database Accession Number: AB000801 & BAA19186. Ichikawa H <i>et al.</i> 27 March 2001. "Oryza sativa mRNA for chalcone synthase, complete cds". See whole document. 76.3% identical to SEQ ID NO: 33.	1-25 (SEQ ID NO: 33 & 77)
X	WO 02/20548, A (Washington State University Research Foundation) 14 March 2002. See whole document., especially SEQ ID NO:25 SEQ ID NO: 25 is 79.3% identical to SEQ ID NO: 33.	1-25 (SEQ ID NO: 33 & 77)
P, X	WO 02/086146, A (Cornell Research Foundation Inc.) 31 October 2002. See whole document. SEQ ID NO: 46 is 92.4% identical to SEQ ID NO: 33.	1-25 (SEQ ID NO: 33 & 77)

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/NZ03/00081

C (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages (Remove spaces when completed if the page is too long)	Relevant to claim No.
X	<p>GENPEPT &amp; GENBANK database Accession Numbers: AAF23859 &amp; AF092912. Devic M <i>et al.</i> 11 January 2000. "DFR-like protein [Arabidopsis thaliana]". See whole document. 45.6% identity &amp; 63.6% similarity with SEQ ID NO: 79 43.2% identity &amp; 67.2% similarity with SEQ ID NO: 81</p>	1-25 (SEQ ID NO: 35 & 79, 37 & 81)
X	<p>GENPEPT &amp; GENBANK database Accession Numbers: CAA75998 &amp; Y16042. Bernhardt J <i>et al.</i> 30 June 1998. "Dihydroflavonol4-reductase [zea mays]". See whole document. 39.3% identity &amp; 61.6% similarity with SEQ ID NO: 79 38.3% identity &amp; 64.7% similarity with SEQ ID NO: 81</p>	1-25 (SEQ ID NO: 35 & 79, 37 & 81)
X	<p>GENPEPT &amp; GENBANK database Accession Numbers: BAA12723 &amp; D85102. Tanaka Y <i>et al.</i> 6 February 1999. "Dihydroflavonol 4-reductase [Rosa hybrid cultivar]". See whole document. 39% identity &amp; 60.9% similarity with SEQ ID NO: 79 40.2% identity &amp; 65% similarity with SEQ ID NO: 81</p>	1-25 (SEQ ID NO: 35 & 79, 37 & 81)

**Supplemental Box**

(To be used when the space in any of Boxes I to VIII is not sufficient)

**Continuation of Box No: II**

The international application does not comply with the requirements of unity of invention because it does not relate to one invention or to a group of inventions so linked as to form a single general inventive concept. The fundamental test for unity of invention is specified in Rule 13.2 of the Regulations under the PCT.

"Where a group of inventions is claimed in one and the same international application, the requirement of unity of invention referred to in Rule 13.1 shall be fulfilled only where there is a technical relationship among those inventions involving one or more of the same or corresponding special technical features. The expression "special technical feature" shall mean those technical features that define a contribution which each of the claimed inventions, considered as a whole, make over the prior art."

In the case of the present application, the problem addressed by the application is the need in the art for materials useful in the modification of fructan and tannin content and composition in plants. The solution provided by the applicant is to provide enzymes involved in the fructan, cellulose, starch and/or tannin biosynthetic pathways isolated from forage grass tissues. Specifically, the solutions provided are in the form of 44 specific enzymes from ryegrass or fescue species and the nucleic acids or fragments coding for these enzymes. These 44 specific polypeptides fall within general groupings dependent upon which pathway they appear in (Table 1 pages 17-21). Such groupings do not confer a "special technical feature" in terms of their function.

The protein groups do share the feature of being from the plant species *Lolium* (ryegrass) or *Festuca* (fescue). However the species of origin can only constitute a special technical feature if the species or origin makes a contribution over the prior art. There is nothing in the application to indicate that isolation of peptides from fescue or ryegrass is inventive. It was known that enzymes belonging to these families would be present in ryegrass and fescue (by analogy with other plant species). The presence of these enzymes in other plant species is known in the prior art.

Therefore, none of the enzymes have any functional feature that can be seen as a "special technical feature" in common. Furthermore, none of the sequences claimed appear to have any significant homology to one another that would provide for a "special technical feature" based upon structure. Finally, none of the sequences claimed can be searched without requiring significant extra effort.

Therefore, this application is directed towards 44 separate inventions. As a service to the Applicant the ISA has searched ten separate inventions for the one fee. The Applicant selected ten sequences to be searched. The ten selected nucleotide sequences and their corresponding protein sequences that were searched are:

SEQ ID NO: 4 and 48

SEQ ID NO: 12 and 56

SEQ ID NO: 15 and 59

SEQ ID NO: 17 and 61

SEQ ID NO: 20 and 64

SEQ ID NO: 22 and 66

SEQ ID NO: 27 and 71

SEQ ID NO: 33 and 77

SEQ ID NO: 35 and 79

SEQ ID NO: 37 and 81.

**PCT/NZ03/00081**

Patent Document Cited in Search Report				Patent Family Member			
(To put a line under the citations tab to the first point on the next row and press F8)							
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WO	200220548	AU	200188741	CA	2421911	US	2002174452
WO	2002086146		NONE				

END OF ANNEX